(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Fri Jun 11 17:13:56 1999; MasPar time 4.85 Seconds 65.804 Million cell updates/sec

Description: Perfect Score: Sequence: >US-08-991-628-1 (1-15) from US08991628 pep 101 ATQKITYRISGVGID 15

Scoring table: PAM 150 Gap 15

Searched: 170751 seqs, 21266608 residues

Pont-processing: Minimum Match 0% Listing first 45 summaries

Database:

-geneseq35
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part24 35:part35 36:part36 37:part37 38:part38

Statistics: Mean 18.436; Variance 54.674; scale 0.337

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	80	ID	Description	Pred. No.
, i	101	100.0	15	20:	W04841	Self epitope of desmo	1.83e-04
2	101	100.0	614	19	W07908		1.83e-04
ω	101	100.0	999	σ	R30742	Human pemphiqus vulga	1.83e-04
4	87	86.1	778	21	W15489	Pemphigus foliaceus a	9.69e-03
₅	57	56.4	1363	27	W31706	Bovine coronavirus E2	2.94e+01
6	57	56.4	1363	N	R11061		2.94e+01
7	54	53.5	878	15	R85487	н	6.20e+01
8	54	53.5	878	10	R55060	Sequence of human liv	6.20e+01
9	53	52.5	309	ب	R06441	MG-6 antigen.	7.93e+01
10	52	51.5	626	30	W37140	Pea plastidial phosph	1.01e+02
11	51	50.5	504	38	W73500	Trabecular meshwork i	1.29e+02
12	51	50.5	504	39	W89391	Human trabecular mesh	1.29e+02
13	51	50.5	504	34	W64669	Human TIGR protein.	1.29e+02
14	51	50.5	504	32	W60670	Human glaucoma associ	1.29e+02
15	51	50.5	504	36	W70496	Trabecular meshwork i	1.29e+02
16	51	50.5	560	24	W13009	Segment of desmosomal	1.29e+02

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70	38	38	38	35	29	4	4	246	40	w	23	7	σ	o	g)	σ	σ	σ	σ	ഗ	6	358	58	87	87	6	16	œ	
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IP3 receptor.	ccharomyces cerevi	ol-delta-14-redu	Cei	n secreted prote	CoA-reduct	nce ei	A reduc		nt of hume	andom biotinylati	tinylation peptid	ant protease (del	t protease (del	ant protease (K74	nt prot	ant protease (Al3	otease (K13	t protease (A	t protease (A	utant protease (del	ris protein	ingivalis hagD h	utini	lvalis haemag	utini	uman ca	5	equence encoded by	0
9e+0	.64e+0	.64e+0	.64e+0	.64e+0	.64e+0	.64e+0	.64e+0	.64e+	.64e+	.64e+	. 64e+	.29e+	.29e+	.29e+	.29e+	.29e+	.29e+	.29e+	.29e+	.29e+	.29e+		.29e+	.29e+	.29e+	.29e+	. 29e	.29e+	

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	derived from the human desmodlein protein are described in WOA841-47.	derived from the human desmoglein 3 protein (amino acids 78-93 (sic))	T-cells in individuals with the autoimmune disease. This peptide is	disease and which binds to the polypeptide to activate autoreactive	protein, such as HLA-DR, which is associated with a human autoimmune	sequence corresponding to a sequence motif for a MHC class II	polypeptide (whether self or non-self) includes an amino acid	tolerising an individual to that polypeptide. In both cases, the	e of	(MBP) polypeptide which is capable of tolerising an individual to an	either an isolated human non-collagen or non-myslin basic protein	Pharmaceutical preparations for tolerisation to antiqens comprise	Claim 1: Page 38: 58pp: English.	•	other self and non-self antigens		Pemphigus vulgaris auto-antigens and multiple sclerosis non-self	/42.	Strominger JL, Wucherpfennig KW;	(HARD) HARVARD COLLEGE.	07-MAR-1995; US-400796.	07-MAR-1996; U03182.	12-SEP-1996.	WO9627387-A1.	Homo sapiens.	influenzā; haemagglutinin; reovirus; sigma protein.	human papillomavirus; Epstein-Barr virus; DNA polymerase;	herpes simplex virus; adenovirus; phosphomannomutase;	pemphigus vulgaris; desmoglein; multiple sclerosis;	autoantigen; HLA; human leukocyte antigen; T-cell; thymocyte;	Tolerisation; self-epitope; antigen; autoimmune disease;	Self epitope of desmoglein 3, implicated in autoimmune disease.	W04641; 18-FEB-1997 (first entry)	W04641 Standard; peptide; 15 AA.	1

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Matches 15; Conservative
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30-JUN-1995; 165632.
30-JUN-1994; JP-173291.
(NISH/) NISHUKAWA T
WPI; 96-388562/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fused protein recognised by pemphigus vulgaris auto:antibody - useful to treat and diagnose pemphis vulgaris Claim 1; Page 7-9; 9pp; Japanese.
W07908 represents the human pemphigus vulgaris (PV) antigén extracellular region. The PV antigen is produced in patients with pemphis vulgaris resulting in autoimmune disease. PV is a rare relapsing disease causing suprabasal, intra-pidermal bullae (vesicles) of the skin and mucuous membranes, which is fatal if untreated. The PV antigen was fused to a human IgGl hinge region and the resulting fusion protein is useful to treat or diagnose
                                                                                                                                                       DNA encoding pemphigus vulgaris antigen - useful in proteins for diagnostic and therapeutic uses Disclosure; Fig 7; SOpp; English.
This sequence is the pemphigus vulgaris 130kD antigen. The protein and its encoding DNA may be used in the diagnosis and treatment of pemphigus vulgaris. It is thought that the antigen may be a cell adhesion molecule.
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27-NOV-1991; US-798918.
(USSH) US DEPT HEALTH &
Amagai M, Klaus-kovtun V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R30742 standard; Protein; 999
R30742;
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Sequence 614 AA;
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Pemphigus vulgaris; skin disease; autoantibodies;
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Autoantibody; immunoglobulin G; IgGl; fusion protein; diagnosis;
treatment; pemphigus vulgaris; PV; bulla; blister; skin disease;
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V, Stanley JR;
      Score 101;
Pred. No. 1.
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0; Mismatches 0;
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This sequence represents a fused protein recognised by pemphigus foliaceus patient autoantibody which comprises the constant region of IgG linked to the extracellular region of pemphigus foliaceus antigen protein through the hinge portion. Pemphigus foliaceus is a chronic, generalised, vesicular and scaling skin eruption similar to dermatitis herpetiformis. The pemphigus foliaceus antigen fusion protein is useful to treat pemphigus foliaceus. The antigen is especially administered through an adsorbent upon which the fusion protein is immunobilised via a carrier. The fusion protein is useful to treat pemphigus foliaceus antibodies which is useful in immunodiagnosis. The fusion protein has little or no side effects.
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Best Local S
Matches 1
                                                        US5672350-A.
30-SEP-1997.
22-AUG-1989;
19-DEC-1991;
22-AUG-1989;
18-OCT-1991;
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12-SEP-1995;
12-SEP-1995;
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Pemphigus foliaceus; autoantibody; constant region;
extracellular region; antigen; hinge portion; skin;
                                                                                                                                                                                                                                                                            Domain
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WPI; 97-241758/22.
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US-811422.
US-397689.
US-779500.
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larity 80.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP-260899
                                                                                                                                                                                                                                                                        /label-
1306..13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens.
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                                                                                                                                                                                                                                            /note-
                                                                                                                                                                                                                                                                                                                                                                 /label=
                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
E2 (S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93
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                                                                                                                                                                                                                                            "transmembrane
                                                                                                                                                                                                                                                                                               Mat_protein
                                                                                                                                                                                                                                                                                                                                                              Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          778
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Pred.
1; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                re 87; DB 21; Le
d. No. 9.69e-03;
Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     spike; antigen;
                                                                                                                                                                                                                                            domain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 778;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches
                                                                    Query Match
Best Local
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10-AUG-1990; CA0252.
22-AUG-1989; US-397689.
(VETE-) VETERINARY INFECTIO.
Parker MD, Cox GJ, Babiuk LA;
WPI, 91-087247/12.
                                                                                                                                                                                                                                                                                                                                                                                                                Bovine Coronavirus E2 protein.
Bovine Coronavirus; BCV; E2; E
Bovine Coronavirus; Quebec is
Key
                                                                                                                                                                                                                                                                                                         WO9102752-A.
                                                                                                       E3 - useful as vaccine component Disclosure; Fig 3 (1-6); 70pp; English.

D1sclosure; Fig 3 (1-6); 70pp; English.

E2 protein is one of the four proteins (N, E1, E2 and E3)

ECV. The E2 and E3 polypeptides, or fragments of these, a subunit antigens in vaccines for protection against or ame BCV, without risk of infection.

Sequence 1363 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coronavirus polypeptide(s)
Claim 13; Fig 3; 52pp; English.
This polypeptide comprises the E2
                                                                                                                                                                                                                                                                                                                                                                           cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R11061;
24-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R11061 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                        Deoxyribonucleic acid encoding Bovine
                                                                                                                                                                                                                         N-PSDB; Q10947.
                                                                                                                                                                                                                                                                                                                                                   domain
                                                                                                                                                                                                                                                                                                                                                                                                        peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccines against bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Babiuk LA, Cox GJ, WPI; 97-488823/45.
                 nvqyringigv 1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nvqyringigv 1005 :: |||:|:|:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KITYRISGVGI
  KITYRISGVGI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 56.4%;
Similarity 45.5%;
5; Conservative
                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1363 AA;
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                           /label- sig_peptide
766..766
                                                                                                                                                                                                                                                                                                                                                /note= "pro
1306..1338
                                                                                                                                                                                                                                                                                                                                                                                                                  us; BCV; E2; E3; vac
us - Quebec isolate
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                     /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein; 1363
                                                                    56.48;
45.5%;
                                                                                                                                                                                                                                                                                                                                                              "probable cleavage site"
                                                                                                                                                                                                                                                                                                                                   transmembrane_domain
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                                                                   Score
Pred.
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Pred.
5; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                E3; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             re 57; DB 27; I
1. No. 2.94e+01;
Mismatches 1;
                                                       Mismatches
                                                                    57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein,
                                                  DB 2; L. 2.94e+01; 1;
                                                                                                                                                                                                         coronavirus
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                                                                                 Length 1363;
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                                                                                                                                                                                                         protein
                                                      Indels
                                                                                                                                      ameliorating
                                                                                                                                                   are
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                                                                                                                                                                                                           E2
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(UYYA) UNIV YALE.
(MOTTOW JS, Rimm DL;
MOTTOW JS, Rimm DL;
MOTTOW JS, Rimm DL;
R N-PSDB; Q65487.
R N-PSDB; Q65487.
T develop prods. for diagnosis, prognosis, therapy and I develop prods. for diagnosis, prognosis, therapy and I for t-cacherin disorders, e.g. malignancies
PS Claim 1; Page 59-63; 97pp; English.
Claim 1; Page 59-63; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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The human E-cadherin protein precursor (R85487) is expressed by an CDNA clone (T05764) derived from human liver. The extracellular domain of E-cadherin is used to generate peptides that specifically bind to heterotypic cognates of E-cadherin and which inhibit adhesion of intra-epithelial T-lymphocytes to E-cadherin expressing epithelial or endothelial cells in vitro or in vivo, thereby modulating nucosal immune responses. Such peptides are also specifically reactive with a monoclonal antibody (E4.6 or E6.1) that binds to E-cadherin and that can inhibit T-cell binding.

Sequence 878 AA;
                                                                                                                                                                                                                                                                                                                                                         08-NOV-1994 (first entry)
Sequence of human liver E-cadherin.
Human epithelial-cadherin; E-cadherin; cell adhesion molecule; CAM; uvomorulin; L-CAM; Cell CAM 120/80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human E-cadherin precursor.
E-cadherin; T-lymphocyte; alpha-E,beta-7 integrin;
autoimmune disease; Crohn disease; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R85487;
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R55060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDb; round adhesion adhesion agents to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-MAY-1994; US-237919.
(BGHM ) BRIGHAM & WOMENS
Brenner MB, Cepek KL;
WPI; 95-392921/50.
                                                                                                                                                                                                                                                    16-NOV-1993;
17-NOV-1992;
                                                                                                                                                                                                                                                                                                                           WO9411401-A.
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09-NOV-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain
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                                                                                                                                                                                                                                                                                                         26-MAY-1994.
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 53.5%;
Similarity 100.0%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note- "the extracellular domain (amino acids of the mature protein) is the preferred region for generation of peptides of the invention"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of T ]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Extracellular_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54;
Pred. No.
0; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 15;
6.20e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E-cadherin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e.g. Crohn's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                    used to prophylaxis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uvomorulin, L-CAM and Cell CAM 120/80. The DNA encoding hEC was obtd. by screening normal human liver and hepatocellular carcinoma cDNA clibraries and a colonic epithelial cell cDNA library. The following sequences are specifically claimed: AAS 1-878; 151-878; 30 sequential AAS from AAS 308-878; AAS 1-150; AAS 178-289; AAS 290-401; AAS 402-513; AAS 178-513; AAS 151-703; AAS 1790-379; AAS 704-878; nucleotide sequences comprising nucleotide numbers life-2749; 566-2749; 1-1053; 510-2696; 1332-3000; 540-1500; 348-906; 890-1648; 384-1208; 641-2046; 685-1335; 880-1661; 1199-1742; 1373-1742; 1705-2204; 2458-2775; DNA encoding at least 30 AAS selected from AAS 308-878. The prods. can be used in the diagnosis, prognosis, therapy and prophylaxis of conditions involving improper E-cadherin expression. Suitable dosages for i.v. admin. of a protein are 50-500 mcg/kg body wt.
                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches
15-JAN-1998.
03-JUL-1997; 1
10-FEB-1997; 09-JUL-1996;
18-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                               plagnostic and vaccine for poultry mycoplasma serum - utilises antigen protein of the disease and recombinant vector incorporated with its coding gene.

Claim 2; Fig 1f; 20pp; Japanese.

DNA encoding the protein can be inserted into an expression vector for the prodn. of MG-1 polypeptide which elicits an antigen-antibody reaction with anti-mycoplasma gallisepticum poultry sera. It may also be ligated to other DNA to produce fusion proteins with an N-terminal
                                                                      rug3 mutation.
Pisum sativum var.
WO9801574-A1.
                                                                                                                                                                                                                                                                                                                                          bacterial enzyme sequence.
See also R05081-2 and R06437-40.
Sequence 309 AA;
                                                                                                                Phosphoglucomutase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MG-6
                                                                                                                               Pea plastidial
                                                                                                                                            06-JUL-1998
                                                                                                                                                           W37140;
                                                                                                                                                                     W37140 standard; Protein; 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; Q05653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUN-1989; 136343.
02-JUN-1989; JP-136343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycoplasma gallisepticum; poultry; vaccine J02111795-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-OCT-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (JAPG) Nippon Zeon KK, NPI; 90-169109/22.
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                                                                                                                                                                                                                                                                                    h 52.5%;
Similarity 58.3%;
7; Conservative
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Similarity 100.0%;
7; Conservative
  ; E03613.
; GB-002653.
; US-021410.
; GB-015103.
                                                                                                                             (first entry)
al phosphoglucomutase
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                                                                                       Novella
                                                                                                                pea;
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                                                                                                                PGM(p);
                                                                                                                                                                                                                                                                                                   Score 53;
Pred. No.
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Pred. No.
0; Misma
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                                                                                                                 sucrose;
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, 7.93e+01;
Thes 2;
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20e+01;
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                                                                                                                transgenic
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RESULTING AND ACCORDANCE OF SOLUTION AND ACCORDA
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Best Local S
Matches
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Best Local Similarity 60.0%;
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(UNIL ) UNILEVER PLC.
                                                                                                                                                                                                                                                                                        glaucoma (Claim 1: Column 25-28; 22pp; English.

This sequence represents the human Trabecular meshwork induced glucocorticoid response (TIGR) protein. The TIGR protein is a secretory protein specifically bound by the antibody of the invention. The antibody, especially in labelled form, can be used in the diagnosis of glaucoma by detecting elevated levels of the protein in the trabecular meshwork of the eye. Using the antibody, glaucoma is detected more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pea seeds lacking plastidial phosphoglucomutase activity - have higher sucrose levels at end of vining period and can be vined over extended period compared to conventional varieties Disclosure; Page 58-62; 83pp; English.

This protein comprises pea plastidial phosphoglucomutase (PGM(p)), an enzyme that catalyses the interconversion of glucose-1-phosphate and glucose-6-phosphate, and is thus involved in starch synthesis. The amino acid sequence was deduced from an isolated cDNA clone (see Y00731) and shows considerable homology to known PGM sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides pea plants that have substantially reduced PGM(p) activity or which substantially lack PGM(p) activity. This may be the result of antisense or sense suppression technology. Pea seeds from such plants have higher sucrose levels at the end of the vining period and may be vined over an extended period compared to conventional varieties. The invention provides pea seeds having a sucrose content of over 6% of total weight, and a ratio of
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N-PSDB; V00731.
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Huang W, Nguyen TD, Polansky
WPI: 99-069807/06.
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03-NOV-1994; US-336235.
20-OCT-1995; US-546568.
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                                                                                                                                                                                                                                                                        accurately.
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Trabecular meshwork induced glucocorticoid response protein
TIGR protein; trabecular meshwork induced glucocorticoid res
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US5849879-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         secretory protein; antibody;
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                                                           281 tgettwridtvgtd
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TOKITYRISGVGID
                                                                                                                       50.5%;
Similarity 57.1%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to trabecular meshwork protein -
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Pred. No. 1.01e+02;
2; Mismatches 2;
                                                                                                                       Score 51; DB 38; Le
Pred. No. 1.29e+02;
0; Mismatches 6;
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RESULT

W89391

standard;

504

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PT New Isolated glaucoma-associated nucleic acids - which encode
PT Trabecular Meshwork Induced Glucocorticoid Response protein, used to
PT develop products for diagnosing glaucoma-related diseases
Claim 1; Fig 1; 22pp; English.
CC The present sequence is a human secretory protein from clone II.2.
CC The secretory protein is designated TIGR (Trabecular Meshwork Induced CG Glucocorticoid Response) protein. The protein is highly induced by
CC glucocorticoids in the endothelial lining cells of the human trabecular
CC meshwork. The TIGR polynucleotides and proteins can be used as markers
CC for the diagnosis of glaucoma, primary open angle glaucoma (POAG),
CC pigmentary glaucoma, and low tension glaucoma and their related
CC diseases. They can also be used to diagnose or protect an individual's
CC sensitivity to elevated intraocular pressure upon administration of
CC steroids such as glucocorticoids or corticosteroids. These products can
CC also be used for diagnosing other diseases or conditions that affect the
CC expression or activity of the protein. The products can also be
CC formulated for administration to patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches
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N-PSDB; V81910.
New isolated glauco
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17-NAY-1996; US-649432.
03-NOV-1994; US-336235.
20-CCT-1995; US-546568.
25-JUN-1997; US-882238.
(REGC ) UNIV CALIFORNIA.
products for diagnosis, prognosis and treatment of glaucoma Claim 48; Fig 8; 105pp; English.

This sequence represents a novel human trabecular meshwork induced glucocorticoid response protein (TIGR) which is used in a method for diagnosing glaucoma in a patient. The method involves the detection of polymorphisms whose presence is predictive of a mutation affecting TIGR response in the patient and can be diagnostic of glaucoma or steroid sensitivity. Base substitutions and base additions upstream of and within TIGR exons can also be used to diagnose glaucoma.
                                                                                                                                                                                                      N-PSDB; V51391.
Use of TIGR nucleic acid
                                                                                                                                                                                                                                                     (REGC ) UNIV CALIFORNIA Chen H, Chen P, Nguyen WPI; 98-427946/36.
                                                                                                                                                                                                                                                                                                                                                                                                                               Human TIGR protein.
TIGR; trabecular meshwork induced glucocorticoid response
diagnosis; glaucoma; polymorphism; steroid sensitivity.
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                                                                                                                                                                                                                                                                                                               30-JUL-1998.
09-JAN-1998; U00468.
09-SEP-1997; US-938669.
28-JAN-1997; US-791154.
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W09832850-A1.
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US5854415-A.
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larity 57.1%;
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Pred. No. 1.29e+02;
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W70496;
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Human glaucoma associated
Glaucoma; GLClA; treatment
                                                                                                                                            Trabecular meshwork induced glucocorticoid response* protein Trabecular meshwork induced glucocorticoid response*; TIGR*;
                                                                                                                                                                                                                                                                                                                                                                                                                                    or predisposition Sequence 504 AA;
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W60670 standard; Protein; 504
                                                                        Peptide
                                                                                           Key
                                                                                                            Homo sapiens
                                                                                                                               human;
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                                                                                                                           glaucoma;
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Similarity 57.1%;
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llarity 57.1%;
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57..60
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                  Mat_protein
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. No. 1.29e+02;
Mismatches 6;
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Modified_site

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New protein induced in trabecular meshwork cells by glucocorticoids

"useful in the diagnosis of glaucoma and related diseases
Sclaim 1; Fig 1A-C; 53pp; English.
CHAIN 1; Fig 1
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07-APR-1997; WO-U05391.

01-APR-1997; WO-U05391.

(REGC) UNIV CALIFORNIA.

Huang W, Nguyen TD, Polansky JR;

WPI; 98-542701/46.
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                                     exceeds the amount disease.
                                                           improved methods and reagents for diagnosing glaucoma and related disorders, such as cardiovascular and immunological diseases that affect expression of TIGR*. A claimed method of diagnosing glaucoma involves determining if the amount of TIGR* present in the HTM exceeds the amount found in an individual not predisposed to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; V33484.
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| note= "consensus leucine zipper unit"
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Query Match Best Local Similarity

50.5%;

Score 51; DB 36; Length 504; Pred. No. 1.29e+02;

Db 281 tgettwridtvgtd 294 || || || || | Qy 2 TQKITYRISGVGID 15

Matches

8

Conservative

0

Mismatches

6.

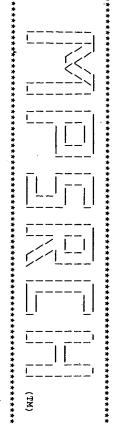
Indels

0;

Gaps

0;

Search completed: Fri Jun 11 17:15:46 1999 Job time: 110 secs.



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:12:13 1999; MasPar time 4.23 Seconds 142.091 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-991-628-1 (1-15) from US08991628.pep 101 1 ATQKITYRISGYGID 15

Scoring table: PAM 150 Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Database:

Statistics: Mean 25.979; Variance 34.700; scale 0.749

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

12 14 15 15 17 19 20 21 22 23	11 987654 110	Result No.
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1363 419 108 108 146 446 479 509 531 882	1043 1043 1043 1049 331 1363 1363 1363 1363	Length
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CLASSIFICATION
KEYWORDS
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                                                                                                                                                                                                                 glycoprotein, as a member of the cadherin family of cell adhesion molecules.
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#cross-references_MUID:92037656
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                                                                                                ##molecule_type mRNA
##residues 44-1001, AOPPSAT' ##label KO3
##cross-references GB:X57784
this sequence has been revised
##note S38721
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##cross-references EMBL:X57784; NID:g436061; PID:g436062
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Biochem. Biophys. Res. Commun. (1990) 173:1224-1230
Desmoglein shows extensive homology to the cadherin
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submitted to the EMBL Data Library, March 1991
Complete sequence of the desmoglein precursor and
for the existence of different desmoglein genes
#superfamily cadherin; cadherin repeat homology
calcium binding; cell adhesion; duplication; glycoprotein;
transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, February 1991 $38721
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Eur. J. Cell Biol.
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S14603
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Wheeler, G.N.; Buxton, R.S.; Parker, A.E.; Rees, D.A.; King, I.A.; Magee, A.I. Biochem. Soc. Trans. (1991) 19:1060-1064 Desmosomal glycoproteins I, II and III: nov
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desmosomal glycoprotein I
#formal_name Homo sapiens #common_name man
30-Jun-1993 #sequence_revision 30-Jun-1993
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J. Cell Sci. (1991) 99:809-821
Structural analysis and expression
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Lenox, A.L.; Graham, D.E.; Overbeek, R.; Sr
Keller, M.; Aujay, M.; Huber, R.; Feldman,
J.M.; Olson, G.J.; Swanson, R.V.
Nature (1998) 392:353-358
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                               *superfamily phosphoribosylformylglycinamidine cyclo-ligase, phosphoribosylformylglycinamidine cyclo-ligase homology
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18-1363
18-768
769-1363
1312-1328
                                                                                                                                                                                                                                                #journal #title
                                                                                                                                                                                                                                                                                 #authors
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Best Local Similarity
                                                                                                                                                                                                                                              #cross-references MUID:90232743
#accession A34607
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                                                                                                                                                  ##molecule_type genomic_RNA
##residues 1-1363 ##label ABR
##coross-references GB:#31053; NID:g323361;
##CTCATION #superfamily coronavirus E2 glyc
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##mollecule_type DNA
##residues 1-441 ##label ROU
##cross-references EMBL:AC003000;
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Similarity 40.0%;
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#length
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2 glycoprotein precursor - bovine coronavirus (strain Mebus)
peplomer glycoprotein; S glycoprotein; spike glycoprotein
90A glycoprotein; 90B glycoprotein
#formal_name bovine coronavirus
#formal_name bovine revision 30-Jun-1991 #text_change
                                                                                                                                                                                                                                                                                     Abraham, S.; Kienzle, T.E.; Lapps, W.; Brian, D.A. Virology (1990) 176:296-301
Deduced sequence of the bovine coronavirus spike protein and identification of the internal proteolytic cleavage site.
                                                                                                                                     glycoprotein; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                   A34607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T01000
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                                                                                                                                                                                                                                                                                                                                                                                                                               20-Mar-1998
#domain signal sequence #status predicted #label SIG\
#product E2 glycoprotein #status predicted #label EGB\
#product 90B glycoprotein #status predicted #label EGB\
#product 90A glycoprotein #status predicted #label EGA\
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58.3%;
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331 #molecular-weight 36768 #checksum
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Pred. No. 1.98e+00;
3; Mismatches 2
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Pred. No. 3.07e+00;
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BAC T517 genomic sequence.
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                                                                                                                                                                                                                                                                                                                            #authors Zhang, X.; Kousoulas, K.G.; Storz, J.
#journal Virology (1991) 183:397-404
#title Comparison of the nucleotide and deduced amino acid sequences
#title of the S genes specified by virulent and avirulent strains
of bovine coronaviruses.
#cross-references_MUID:91272503
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18-768
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##status preliminary

##molecule_type DNA

##residues_ 1-1363 ##label KUE

##cross-references EMBL:232769; NID:9475893; PID:9475894

##cross-references EMBL:232769; NID:9475894

##cross-references EMBL:232769; NID:9475893; PID:94758
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                                                                                                                                                            ##residues 1-1363 ##label ZHA
##cross-references GB:M64667; NID:g323355; PID:g323356
FICATION #superfamily coronavirus E2 glycoprotein
                                                                                                                                                                                                                                                               ##molecule_type genomic RNA
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Local Similarity 45.5%;
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E2 glycoprotein precursor - bovine coronavirus (strain I
peplomer glycoprotein; S glycoprotein; spike glycoprotei
90A glycoprotein; 90B glycoprotein
#formal_name bovine coronavirus
30.Jun-1992 #sequence_revision 30.Jun-1992 #text_change
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submitted to the EMBL Data Library, April 1994
Sequence and functional analysis of the surface protein two human Coronavirus OC43 isolates adapted to growth MDCK I and Vero cells.

$44241
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surface protein - human coronavirus
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13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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#domain signal sequence #status predicted #label SIG\
#product E2 glycoprotein #status predicted #label E2G
#product 90B glycoprotein #status predicted #label EG
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transmembrane protein
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Pred. No. 3.07e+00;
5; Mismatches 1
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739,788,895,937,
1194,1224,1234,
1253,1267;1288
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18-1363
18-768
769-1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors Parker, M.D.; Yoo, D.; Cox, G.J.; Babiuk, L.A.
#journal J. Gen. Virol. (1990) 71:263-270
#title Primary structure of the S peplomer gene of bovine
coronavirus and surface expression in insect cells.
#cross-references MUID:90171910
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                                                                                                                                                                                                                                                       59,133,198,359,437,
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KITYRISGVGI
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                                                                                        similarity 45.5%;
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Similarity 45.5%;
5; Conservative
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predicted
#length 1363 #molecular-weight 150868 #^hortenm 6001
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90A glycoprotein; 90B glycoprotein
#formal_name bovine coronavirus
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                                                                       Conservative
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#product E2 glycoprotein #status predicted #label E9B\
#product 90B glycoprotein #status predicted #label E9B\
#product 90A glycoprotein #status predicted #label E9A\
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KEYWORDS
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937,1194,1224,1234,
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1-1363 ##label BOI
#+cross-references GB:DO0731; NID:g221136; PID:d1001089; PID:g221137
##CCATION #superfamily coronavirus E2 glycoprotein
#BOS glycoprotein; peplomer protein; spike protein; transmembrane
                                                                                             ##molecule_type genomic RNA
##residues 1-1363 ##label ZHA
                                                       ##cross-references GB:M64668
FICATION #superfamily coronavirus E2
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KITYRISGVGI 14
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5; Conservation
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and mouse hepatitis virus strains.
                                                                                                                                           B40320
                                                                                                                                                                                              Zhang, X.; Kousoulas, K.G.; Storz, J.
Virology (1991) 183:397-404
Comparison of the nucleotide and deduced amino acid sequences
of the S genes specified by virulent and avirulent strains
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90A glycoprotein; 90B glycoprotein
#formal_name bovine coronavirus
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
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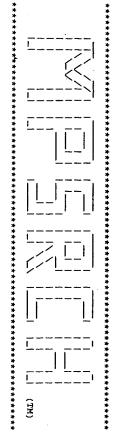
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444,649,676,696,
714,739,788,895,
937,1194,1224,1234,
                                                                        #accession
                                                                                     #title Comparison of the nucleotide and deduced amino acid sequences of the S genes specified by virulent and avirulent strains of bovine coronaviruses.

**cross-references MUID:91272503**
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##cross-references EMBL:233768; NID:9475891; PID:9475892
FICATION #superfamily coronavirus E2 9lycoprotein
RY #length 1363 #molecular-weight 150701 #checl
                                ##molecule_type_genomic RNA
##residues 1-1363 ##label ZHA
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submitted to the EMBL Data Library, April 1994
Sequence and functional analysis of the surface protein
two human Coronavirus OC43 isolates adapted to growth
MDCK I and Vero cells.
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surface protein - human coronavirus
#formal_name human coronavirus
13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
08-Sep-1997
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Virology (1991) 183:397-404
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90A glycoprotein; 90B glycoprotein
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#product 90B glycoprotein #status predicted #label EGB\
#product 90A glycoprotein #status predicted #label EGA\
                                                                                                                                                                                                                                                               _name bovine coronavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  predicted
 coronavirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 57; DB 2; L
Pred. No. 3.07e+00;
5; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 57; DB 1; I Pred. No. 3.07e+00;
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                                                                                                                                                                                                                                                                                90B glycoprotein
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E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 1363;
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glycoprotein
                                                                                                                                                                            Storz,
                                                                                                                                                                                                                                                                                                                                    bovine coronavirus (strain
                                                                                                                                                                                                                                                 30-Jun-1992
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                                                                                                                                                                                                                                                                                                  glycoprotein
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                                                                ALTERNATE_NAMES
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 55.4%;
Best Local Similarity 38.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 56.4%;
Best Local Similarity 45.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            burgdorferi.
#cross-references MUID:98065943
#accession D70163
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:: |||:|:|:
4 KITYRISGYGI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                  278 RNIAYRINNINVD 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *#6xperimental_source strain B31
(Y .#length 419 #molecul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133,198,359,437,
                                                                                                                                                                                                                                                                                                                                                          3 QKITYRISGVGID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,1267,1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39,788,895
                                                                               hypothetical 11.6K protein -
edge-associated virus
ORF3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Hor K.; Roberts, K.; Hatch, B.; Smith, H.O.; Venter, J.C. Nature (1997) 390:580-586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.; Dodson, R.; Hickey, E.K.; Gwlinn, M.; Dougherty, B.; Tomb, J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.; J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.; Weidman, Vugt, R.V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weidman, J.; Utterback, T.; Watthey, L.; McDonald, L.; Artiach, P.; Bowman, C.; Galland, S.; Fujil, C.; Cotton, M.D.; Horst, W. Bowman, C.; Galland, S.; Fujil, C.; Cotton, M.D.; Horst, Vugt, R.V.; Palmer, N. S.; Pujil, C.; Cotton, M.D.; Horst, V. S.; Pujil, C.; Cotton, M.D.; Pujil, C.; Cotton, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D70163 #type complete
hypothetical protein BB0509 - Lyme disease spirochete
#formal_name Borrelia burgdorferi #common_name Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #length 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glycoprotein; transmembrane protein
#formal_name strawberry mild yellow edge-associated virus
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
31-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eb-1998 #sequence_revision 13-Feb-1998 #text_change
-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #domain signal sequence #status predicted #label SIG\
#product E2 glycoprotein #status predicted #label EGB\
#product 90B glycoprotein #status predicted #label EGB\
#product 90A glycoprotein #status predicted #label EGA\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *domain transmembrane #status predicted #label TMN\
                                                                                                                                                                                                                                                                                                                                                             15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #molecular-weight 48741 #checksum
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Pred. No. 3.07e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 56; DB 2; I
Pred. No. 4.74e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                   strawberry mild yellow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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KEYWORDS
SUMMARY
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                                    밁
                                                                                      Query Match 54.5%;
Best Local Similarity 58.3%;
                                                                       Matches
                                                                                                                                                                                                                                                                                 #authors Jelkmann, W.; Maiss, E.; Martin, R.R.
#journal J. Gen. Virol. (1992) 73:475-479
#title The nucleotide sequence and genome organization
mild yellow edge-associated potexvirus.
#cross-references MUID:92166762
                                                                                                                                                                                                                                                                 #accession
                                                                                                                                                                            PID:g222634 **experimental_source strain MY-18
                                                                                                                                                                                                           ##molecule_type genomic RNA
##residues 1-108 ##label
##cross-references GB:D12517;
9 HSITYRILAVGL 20
: |||| :||:
3 QKITYRISGVGI 14
                                                                                                                                         #length 108 #molecular-weight 11589
                                                                                                                                                            transmembrane protein
                                                                       Conservative
                                                                   Score 55; DB 2;
Pred. No. 7.28et
3; Mismatches
                                                                                                                                                                                                          JEL DDBJ:D01227; NID:g222631; PID:d1002574;
                                                                                      55; DB 2; I
No. 7.28e+00;
                                                                                                        Length 108
                                                                       Indels
                                                                                                                                           #checksum
                                                                       0
                                                                                                                                           628
                                                                                                                                                                                                                                                                                                                        of strawberry
                                                                     Gaps
                                                                       0
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Search completed: Fri Jun 11 17:13:37 1999 Job time: 84 secs.



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Fri Jun 11 17:09:17 1999; MasPar time 2.55 Seconds 166.490 Million cell updates/sec

Description: Perfect Score: Title: >US-08-991-628-1 (1-15) from US08991628.pep 101 1 ATOKITYRISGVGID 15

Scoring table: PAM 150 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum.Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 26.539; Variance 30.462; scale 0.871

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	л 5 3 . л 5	52.5	52.5	53.5	53.5	53.5	53.5	53.5	54.5	54.5	54.5	54.5	56.4	56.4	56.4	56.4	56.4		61.4	86.1	86.1	100.0	; -	Query
, 0	1235	890	543	884	882	531	509	479	897	446	169	108	1363	1363	1363	1363	1363	1363	388	1049	1043	999	Length I	
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AGEA TO A BOC	VGL2_CVMJH	BCN5_CLOPE	YDE3_SCHPO	CAD1_MOUSE	CAD1_HUMAN	GSPE_XANCP	CRU3_BRANA	CRU1_RAPSA	BGAL_CLOAB	AP50_SCHPO	Y459_MYCPN	VMEM_SMYEA	VGL2_CVBL9	VGL2_CVBF	VGL2_CVBV	VGL2_CVBQ	VGL2_CVBLY	VGL2_CVBM	PUR5_VIGUN	DSG1_HUMAN	DSG1_BOVIN	DSG3_HUMAN	Ħ	
EZ GHICOPROTEIN PRECUR	GLYCOPROTEIN	BACTERIOCIN BCN5.	HYPOTHETICAL 61.8 KD P	EPITHELIAL-CADHERIN PR	EPITHELIAL-CADHERIN PR	GENERAL SECRETION PATH	CRUCIFERIN CRU1 PRECUR	CRUCIFERIN PGCRURSE5 P	BETA-GALACTOSIDASE (EC	PUTATIVE CLATHRIN COAT	HYPOTHETICAL PROTEIN M	Ħ	E2 GLYCOPROTEIN PRECUR	GLYCOPROTEIN	E2 GLYCOPROTEIN PRECUR	E2 GLYCOPROTEIN PRECUR	E2 GLYCOPROTEIN PRECUR	E2 GLYCOPROTEIN PRECUR	PHOSPHORIBOSYLFORMYLGL	DESMOGLEIN 1 PRECURSOR	DESMOGLEIN 1 PRECURSOR	DESMOGLEIN 3 PRECURSOR	Description	
). 14e+00	5.14e+00	5.14e+00	;_	٠	٠		'n				1.99e+00			7.46e-01			7.46e-01	. 4 6e	.81e		•	. 98	Pred. No.	

	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
	51	51	51	51	51	51	51	51	51	51	51	51	51	52	52	52	52	52	52	53	53	53
	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	51.5	51.5	51.5	51.5	51.5	51.5	52.5	52.5	52.5
	1902	1711	1709	1271	1218	916	913	887	513	504	493	465	89	1324	1319	1121	956	435	243	1376	1376	1371
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	P2P_LACPA	CHD1_MOUSE	CHD1_HUMAN	BCR_HUMAN	YK83_YEAST	CAD4_HUMAN	CAD4_MOUSE	CAD1_CHICK	IMDH_BACSU	MYOC_HUMAN	IMDH_STRPY	YB57_YEAST	S3AC_BACSU	VGL2_CVMA5	DYNA_DROME	YJ09_YEAST	TSP3_MOUSE	HFE1_HAEIN	TONB_KLEPN	VGL2_CVM4	VGL2_CVMJC	PUR2_CHITE
•	PII-TYPE PROTEINASE PR	CHROMODOMAIN-HELICASE-	CHROMODOMAIN-HELICASE-	BREAKPOINT CLUSTER REG	PROBABLE ATP-DEPENDENT	RETINAL-CADHERIN PRECU	RETINAL-CADHERIN PRECU	EPITHELIAL-CADHERIN PR	INOSINE-5'-MONOPHOSPHA	MYOCILIN PRECURSOR (TR	INOSINE-5'-MONOPHOSPHA	HYPOTHETICAL 51.5 KD P	STAGE III SPORULATION	E2 GLYCOPROTEIN PRECUR	150 KD DYNEIN-ASSOCIAT	HYPOTHETICAL 127.4 KD	THROMBOSPONDIN 3 PRECU	MINOR FIMBRIAL SUBUNIT	TONB PROTEIN.	E2 GLYCOPROTEIN PRECUR	E2 GLYCOPROTEIN PRECUR	PHOSPHORIBOSYLAMINEG
	1.30e+01	1.30e+01	1.30e+01	1.30e+01	1.30e+01	1.30e+01	1.30e+01	1.30e+01	1.30e+01	1.30e+01	1.30e+01	1.30e+01	1.30e+01	8.19e+00	8.19e+00	8.19e+00	8.19e+00	8.19e+00	8.19e+00	5.14e+00	5.14e+00	5.14e+00

ALIGNMENTS

FILAMEN'S MEDIATING CELL-CELL ADHESION. -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. -I- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL, OESOPHAGUS CARCINOMAS.	- CEI	MEI AMA	DSG3 HOMO EUKAF PRIMA	DE 01	ESULT
FILAMENTS N SUBCELLULAR TISSUE SPEC	garis, a c L 67:869-8	[1] SEQUENCE FROM N.A. MEDLINE; 92069753. AMAGAI M., KLAUS-K "Autoantibodies and	DSG3. HOMO SAPIENS (HUMAN). EUKARYOTA; METAZOA; C PRIMATES; CATARRHINI;	P32926; 01-OCT-1993; 01-OCT-1993; 01-NOV-1997; DESMOGLEIN 3	DSG3_HUMAN
FILAMENTS MEDIATING CELL-CELL ADHESION	vulgaris, a disease of cell adhesion."; CELL 67:869-877(1991)INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDI	[1] SEQUENCE FROM N.A. MEDLINE; 92069753. MEDLINE; 92069753. "ALTOPITION OF TRANSPORTED TO THE PROPERTY J.R.;	DSG3. HOMO SAPIENS (HUMAN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.	P32926; 01-OCT-1993 (REL. 27, CREATED) 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) DESMOGLEIN 3 PRECURSOR (130 KD PEMPHIGUS VULGARIS ANTIGEN) (PVA).	STANDARD;
PE I MEME PERMIS, TO	adhesion. NTERCELLU	STANLEY J	VERTEBF	D) SEQUENCE UNNOTATION KD PEMPHI	PRT;
RANE)NGUE,	"; LAR I	. R	ŁΑΤΑ;).	PDATE	999 AA.
PROTEIN. TONSIL,	PROTEINS	0 0 0 0 0 1	MAMMALIA;	TE) ULGARIS F	Α.
OESOPHAGUS AND	aris, a disease of cell adhesion."; 67:869-877(1991). FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE		; EUTHERIA;	ANTIGEN) (PVA).	

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DISEASE: PENDHIGUS VULGARIS (PV) IS A POTENTIALLY LETHAL SKIN DISEASE IN WHICH EPIDERMAL BLISTERS OCCUR AS THE RESULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3. SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS TO THE DESMOSOMAL SUBFAMILY.

EMBL; M76482; G190752; -. PIR; A41088; IJHUG3. MIM; 169615; -. PS00232; CADHERIN; 3 PFAM; PF00028; Cadherin; 4. HSSP; P09803; 1EDH. ω

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SEQUENCE OF 44-455 F.V...

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MEDLINE; 91097553.

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01-OCT-1993 (REL. 27, LA
01-NOV-1997 (REL. 35, LA
DESMOGLEIN 1 PRECURSOR (
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KOCH P.J., GO
FRANKE W.W.;
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CARBOHYD
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SEQUENCE
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"Identification of desmogle:
glycoprotein, as a member oo
molecules.";
EUR. J. CELL BIOL. 53:1-12(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-MUZZLE EPITHELIUM;
MEDLINE; 91168965.
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SUBMITTED (
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BOS TAURUS
                                                                                                                                                                                                                                                       "Complete amino acid sequence of the epidermal desmoglein precursor polypeptide and identification of a second type of desmoglein gene.", polypeptide and identification of a second type of desmoglein gene.", polypeptide and identification of a second type of desmoglein gene.", I
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Q03763;
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EUKARYOTA; METAZOA; CHORD;
ARTIODACTYLA; RUMINANTIA;
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ISSUE-MUZZLE EPITHELIUM;
OCH P.J., GOLDSCHMIDT M.
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Similarity 100.0%;
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ANTIA; PECORA; BOVOIDEA; BOVIDAE;
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TISSUE-KERATINOCYTES;
MEDLINE; 91271279_.
WHEELER G.N., PARKER A.E.,
ARNEMANN J., RUTMAN A.J., E
BUXTON R.S., MAGEE A.I.;
                                                                                                                                                                                DSG1_HUMAN
Q02413;
Q1-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as for emodified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                            DESMOGLEIN 1
                                                                                                                                                           01-OCT-1993
01-NOV-1997
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HSSP; P09803; 1EDH.
CELL ADHESION; SIGNAL; TI
                                                                                                                    HOMO SAPIENS
                                                                EQUENCE FROM N.A.
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TISSUE SPECIFICITY: EPIDERMIS, MUZZLE, TONGUE AND OESOPHAGUS
DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
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SIMILARITY: BELONGS TO
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                                                                                          CATARRHINI;
                                                                                                       NS (HUMAN).
METAZOA; CHORDATA;
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larity 80.0%;
Conservative
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R (DESMOSOMAL GLYCOPROTEIN
                                                                                           HOMINIDAE;
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              , THOMAS
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Pred. No.
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PROC. NATL. ACAD. SCI. U.S.A. 88:4796-4800(1991).
-i- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNION TOLOUTED IN THE INTERACTION OF PLAQUE PROTEINS AND FILAMENTS MEDIATING CELL-CELL ADHESION.
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSILAND O DOMALN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE
PUR5.
VIGNA UNGUICULATA (COWPEA).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYGEUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; FABALES; FABACEAE; PAPILIONOIDEAE; VIGNA
                                                                                         LT 4
PURS_VIGUN STANDARD; PRT; 388 AA.
P52424;
P52424;
01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LICASE PRECURSOR (EC 6.3.3.1)
CAIRS) (PHOSPHORIBOSYL-AMINOIMIDAZOLE SYNTHETASE) (AIR SYNTHASE).
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                                       EMBRYOPHYTA;
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P15777;
01-APR-1990
01-APR-1990
01-JUN-1994
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                                                                                                                                                                                                                                      ABRAHAM S., KIENZLE T.E., LAPPS W.E., BRIAN D.A.;
"Sequence and expression analysis of potential nor
of 4.9, 4.8, 12.7, and 9.5 kDa encoded between the
protein genes of the bovine coronavirus.";
VIROLOGY 177:488-495(1990).
-1- FUNCTION: THE BEPLOWER PROTEIN MEDIATES THE B:
TO THE HOST CELL RECEPTOR AND IS INVOLVED IN N
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SMITH P.M.C., MANN A.J., HALL D.J., ATKINS C.A.;
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DARA BANKS.
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DARA BANKS.
-I- CATALYTIC ACTIVITY: AFP + 5'-PHOSPHORIBOSYL-FORMYLGLYCINAMIDINE
ADP + ORTHOPHOSPHARE + 5'-PHOSPHORIBOSYL-5-AMINOIMIDAZOLE.
-I- PATHWAY: FIFTH STEP IN DE NOVO PURINE BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 90237243.
BRAHAM S., KIENZLE T.E., LAPPS W.E., BRIAN D.A.;

**BRAHAM S., KIENZLE T.E. LAPPS W.E., BRIAN D.A.;

**Deduced sequence of the bovine coronavirus spike protein and identification of the internal proteolytic cleavage site.";

**VIROLOGY 176:296-301(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BOVINE CORONAVIRUS (STRAIN MEBUS).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES,
CORONAVIRIDAE; CORONAVIRUS.
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PFAM; PF00586; AIRS; 1
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-!- SUBLEARITY: TO OTHER AIRS FROM BACTERIA AND EUKARYOTES.
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SEQUENCE FROM N.A.
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1 ATQKITYRISGVGID 15
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-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
-UN-1994 (REL. 29, LAST ANNOTATION UPDATE)
GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN)
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Best Local S
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MEDILINE; 91272503.

ZHANG X., KOUSOULAS K.G., STORZ J.;

ZHANG X., KOUSOULAS K.G., STORZ J.;

"Comparison of the nucleotide and deduced amino acid sequences of t

S genes specified by virulent and avirulent strains of bovine

coronaviruses.";

VIROLOGY 183:397-404(1991).

TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION.
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, M31054; G323364;
A34607; VGIHNM.
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POSITIVE-STRAND VIRUSES,
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SPIKE E2 GLYCOPROTEIN.

SPIKE PROTEIN S1 (90B).

SPIKE PROTEIN S2 (90A).

EXTRACELLULAR (POTENTIAL).
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    GLYCOPROTEIN;
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                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDILINE; 90171910.

PARKER M.D., YOO D., COX G.J., BABIUK L.A.;

"Primary structure of the S peplomer gene of bovine coronavirus surface expression in insect cells.";

J. GEN. VIROL. 71:263-270(1990).

-I- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRIO TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION
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P25193;
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DOMAIN
                                                                                   PIR;
                                                                                                   EMBL;
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VIRUSES; SSRNA POSITIVE-STRAND VIRUSES,
CORONAVIRIDAE; CORONAVIRUS.
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01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN)
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PROTEIN; TRANSMEMBRANE; SIGNAL POTENTIAL.
SPIKE E2 GLYCOPROTEIN.
SPIKE PROTEIN S1 (90B).
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Pred. No. 7.46e-1
5; Mismatches
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SPIKE PROTEIN S1 (90B).
SPIKE PROTEIN S2 (90A).
EXTRACELLULAR (POTENTIAL)
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W; 006A5E61 CRC32;
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                                                                                                                                                                                                                                                                                                 HE BINDING OF VIRIONS IN MEMBRANE FUSION.
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VIROLOGY 183:397-404 (1991).

-1- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRIONS TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION.
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PZ5194;
01-MAY-1992 (REL. 22, CREATED)
01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN)
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ZHANG X., KOUSOULAS K.G., STOR "Comparison of the nucleotide "Comparison of the virulent s genes specified by virulent
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                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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VIRUSES; SSRNA POSITIVE-STRAND VIRUSES,
CORONAVIRIDAE; CORONAVIRUS.
                                                                                                         SIGNAL
                                                                                                                          GLYCOPROTEIN;
                                                                                                                                                                     EMBL; M64668;
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similarity 45.5%;
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SPIKE E2 GLYCOPROTEIN
SPIKE PROTEIN S1 (90B).
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EXTRACELLULAR (POTENTIA
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(POTENTIAL).
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MEDLINE; 90171938.
BOIREAU P., CRUCIERE C., LAPORTE J.;
"Nucleotide sequence of the 9lycoprotein S gene
coronavirus and comparison with the S proteins c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGL2_CVBF STANDARD; PRT; 1363 AA. P25190; PR
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                                                                                                                                                                                                                                                                                                                                                                                                                               virus strains.";
J. GEN. VIROL. 71:487-492(1990).
-!- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRIONS
TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BOVINE CORONAVIRUS (STRAIN F15)
VIRUSES; SSRNA POSITIVE-STRAND
CORONAVIRIDAE; CORONAVIRUS.
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Similarity 45.5%;
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Pred. No. 7.46e-01;
5; Mismatches 1
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EXTRACELLULAR POTENTIAL.
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SPIKE E2 GLYCOPROTEIN.

SPIKE PROTEIN S2 (90A)

SPIKE PROTEIN S2 (90A)
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MEDLINE; 91272503.

ZHANG X., KOUSOULAS K.G., STORZ J.;

ZHANG X., KOUSOULAS K.G., STORZ J.;

"Comparison of the nucleotide and deduced amino acid sequences of t

"Comparison of the nucleotide and avirulent strains of bovine

S genes specified by virulent and avirulent strains of bovine

coronaviruses.";

VIROLOGY 183:397-404 (1991).

-I- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRIONS

-I- FUNCTION: CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION.
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P25191;
01-MAY-1992 (REL. 22, CREATED)
01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PEPLOMER PROTEIN).
                                                                                                                            EMBL; M64667; G323356; -. PIR; A40320; VGIHL9.
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                                                                                                                    GLYCOPROTEIN;
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                                                        SPIKE E2 GLYCOPROTEIN.
SPIKE PROTEIN S1 (90B).
SPIKE PROTEIN S2 (90A).
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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Pred. No. 7.46e-01;
5; Mismatches 1
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                                                (POTENTIAL)
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JELKMANN W., MAISS E., MARTIN R.R.;
JELKMANN W., MAISS E., MARTIN R.R.;
JELKMANN W., MAISS E., MARTIN R.R.;

"The nucleotide sequence and genome organization of strawberry mil
yellow edge-associated potexvirus.";

J. GEN. VIROL. 73:475-479(1992)

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

-!- SIMILARITY: TO ORF3 PROTEIN FROM OTHER POTEXVIRUSES AND TO 12
PROTEIN FROM CARLAVIRUSES.
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PIR; JQ1428; JQ1428.
PFAM; PF01307; Plant_vir_prot;
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01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 35, LAST ANNOTATION UPDATE)
01-OCT-1994 (REL 30, LAST ANNOTATION UPDATE)
11.5 KD MEMBRANE PROTEIN (ORF 3).
STRAWBERRY MILD YELLOW EDGE-ASSOCIATED VIRUS (SMYEAV).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; POTEXVIRUS.
                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pred. No. 1.99e+00;
3; Mismatches 2
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5; Mismatches 1
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W; 54233485 CRC32;
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Best Local S
Matches
                                                                                                                                                               A DEVLIN K., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;

SUBMITTED (JUL-1995) TO EMBL/GENBANK/DBJ DATA BANKS.

SUBMITTED (JUL-1995) TO EMBL/GENBANK/DBJ DATA BANKS.

C. SUBMITTED (JUL-1995) TO EMBL/GENBANK/DBJ DATA BANKS.

C. TO RECEPTORS IN COATED VESICLES. CLATHRIN-ASSOCIANED PROTEIN

C. COMPLEXES ARE BELLEVED TO INTERACT WITH THE CYTOPLASMIC TAILS OF COMPLEXES ARE BELLEVED TO INTERACT WITH THE CYTOPLASMIC TAILS OF MEDICAL STATES.

C. MEMBRANE PROTEINS, LEADING TO THEIR SELECTION AND CONCENTRATION.

C. AP50 IS A SUBUNIT OF THE PLASMA MEMBRANE ADAPTOR (POTENTIAL).

C. SUBUNIT: ASSEMBLY PROTEIN COMPLEX 2 (AP-2) IS AN HETEROTETRAMER COMPOSED OF TWO LARGE CHAINS (ALPHA AND BETA), A MEDIUM CHAIN (API) (BY SIMILARITY).

C. SUBCELLULAR LOCATION: COMPONENT OF THE COAT SURROUNDING THE CYTOPLASMIC FACE OF COATED VESICLES IN THE PLASMA MEMBRANE (BY SIMILARITY): BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS

C. SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANOTATION UPDATE)
PUTATIVE CLATHRIN COAT ASSEMBLY PROTEIN AP50 (CLATHRIN COAT ASSOCIATED PROTEIN AP50) (PLASMA MEMBRANE ADAPTOR AP-2 50 KD PROTEIN) (HA2 50 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 MEDIUM CHAIN).
SPAC31A2.09C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
SCHIZOSACCHAROMYCES.
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HIMMELREICH R., HILBERT H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-ATCC 29342 / M129; MEDLINE; 97105885.
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BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; MOLLICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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01-NOV-1997 (REL. 35, LAST
01-NOV-1997 (REL. 35, LAST
HYPOTHETICAL PROTEIN MG459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AP50_SCHPO
Q09718;
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Local Similarity 46.7%;
les 7; Conservative
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LAST SEQUENCE UPDATE)
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MG459 HOMOLOG.
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Pred. No. 1.99e+00
4; Mismatches
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Matches
                                     Query Match 54.5%;
Best Local Similarity 72.7%;
Matches 8; Conservative
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STRAIN=NCIB 2951;
MEDLINE; 91216979.
HANCOCK K.R., ROCKMAN E
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P24131;
01-MAR-1992 (
01-FEB-1996 (
01-FEB-1996 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                               HYDROLASE;
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                    "Expression and nucleotide sequence of the Clostridium acetobutylicu beta-galactosidase gene cloned in Escherichia coll.";
J. BACTERIOL. 173:3084-3054(1991).
-I- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-GALACTOSIDES.
-I- INDUCTION: LATE IN THE ABE (ACETONE, BUTANOL, AND ETHANOL)
FERMENTATION AND SUBJECT TO GLUCOSE REPRESSION.
-I- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z50113; G914887; -.

PROSITE; PS00990; CLAT_ADAPTOR_M_1; 1.

PROSITE; PS00991; CLAT_ADAPTOR_M_2; 1.

PFAM; PF00928; Adap_comp_sub; 1.

HYPOTHETICAL PROTEIN; COATED PITS.

SEQUENCE 446 AA; 50821 MW; C97D83CC
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                                                                                                                                                        HSSP;
                                                                                                                                                                      PFAM;
                                                                                                                                                                                EMBL; M35107; G144746; -.

PIR; A39405; A39405.

PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1;

PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCOTT D.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLOSTRIDIUM.
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828 KITYEVSGEGI 838
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P00722; 1
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                                                                                              459
503
897
                                                                                                                            GLYCOSIDASE.
459 459
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(REL. 33, LAST SEQUENCE UPDATE)
(REL. 33, LAST ANNOTATION UPDATE)
OSIDASE (EC 3.2.1.23) (LACTASE).
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105020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YOUNG C.A., PEARCE L., MADDOX I.S.,
                                                                                                 MW;
                                      Score 55; DB 1; I
Pred. No. 1.99e+00;
1; Mismatches 2
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Pred. No. 1.99e+00;
1; Mismatches 2;
                                                                                              PROTON DONOR (BY SIMILARITY)
NUCLEOPHILE (BY SIMILARITY).
W; 5CFF268B CRC32;
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4 KITYRISGVGI 14

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RESULT 15
ID CRU1_RAPSA STANL...
AC 002498;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DT 01-NOV-1997 (REL. 35, PRECURSOR (11S GLOBULIN) (12S STORAGE PROTEIN).
CRUCIFERIN PGCRURSE5 PRECURSOR (11S GLOBULIN) (12S STORAGE PROTEIN).

""" 'REPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; ROSIC
                                                                                  ٥
Search completed: Fri Jun 11 17:09:28 1999 Job time: 11 secs.
                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 53.5%;
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                     CHAIN
DISULFID
DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SERAIN-CV. SAXA KNACKER;
MEDLINE; 93043037.

MEDLINE; 93043037.

DEPIGINY-THIS D., RAYNAL M., ASPART L., DELSENY M., GRELLET F.;

"The cruciferin gene family in radish.";

PLANT MOL. BIOL. 20:467-479(1992).

-!- FUNCTION: THIS IS A SEED STORAGE PROTEIN.

-!- SUBUNIT: HEXAMER; EACH SUBUNIT IS COMPOSED OF AN ACIDIC AND A BASIC CHAIN DERIVED FROM A SINGLE PRECURSOR AND LINKED BY A DISULFIDE BOND.

-!- SIMILARITY: BELONGS TO THE 11S SEED STORAGE PROTEINS (GLOBULINS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAPPARAUS SATIVUS (RADISH).

RAPHANUS SATIVUS (RADISH).

EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;

EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;

CAPPARALES; BRASSICACEAE; RAPHANUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X59808; G21118; -.
                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S26223; S26223.
PROSITE; PS00305; 11S_SEED_STORAGE; 1.
                                                                              92 SSPKIAYVVQGMGI 105
:: ||:| : |:|
1 ATQKITYRISGVGI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAMILY.
                                                                                                                                                                                                                                                                              PF00190; Seedstore_11s; 1.

PF00190; Seedstore_11s; 1.

STORAGE PROTEIN; SIGNAL; MULTIGENE FAMILY.

L 1 23 BY SIMILARITY.

L 24 289 CRUCIFERIN PGCRURSE5 ALPHA CHAIN.

CRUCIFERIN PGCRURSE5 BETA CHAIN.

PRID 113 296 INTERCHAIN (ALPHA-BETA) (POTENTIAL).

LETD 113 296 INTERCHAIN (ALPHA-BETA) (POTENTIAL).

LETD 113 141 GLN/GLY-RICH.
                                                                                                                                                                                                                                                     211
479 AA;
                                                                                                                                                                                                                                                   218 P
53256 MW;
                                                                                                                                                            Score 54; DB 1; Length 479; Pred. No. 3.21e+00; 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                            POLY-GLN
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm MasPar time 6.16 Seconds 132.927 Million cell updates/sec

Fri Jun 11 17:09:46 1999;

Tabular output not generated.

hate out

Description: Perfect Score: Sequence: Title: >US-08-991-628-1 (1-15) from US08991628.pep 101

ATQKITYRISGVGID 15

Scoring table: PAM 150 Gap 15

179066 segs, 54579741 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl9
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 25.479; Variance 31.590; scale 0.807

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22121111111111111111111111111111111111	Result
5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	Score
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Query Match
993 3380 2269 331 441 1363 1363 1363 1363 1419 108 878 878 878 82 82 82 82 82 82 82 82 82 82 82 83 84 84 86 87 87 88 87 88 87 88 87 88 87 88 87 88 87 88 87 88 87 88 87 88 87 88 87 88 87 88 88	Length
2237775425444	DB
035902 024292 077360 077360 066968 066291 066290 051462 041278 0241278 0241278 0241278 0215855 015855 015855 015855 015855 015855 015855 015855 015853 01585	ID
DESMOGLEIN 3 (FRAGMENT ADMERIN. MAL3P4.25 PROTEIN. PHOSPHORIBOSYLFORWYLGI T517.1 PROTEIN PRECUR SURFACE PROTEIN PRECUR SURFACE PROTEIN PRECUR FAGIO.3 PROTEIN. CHITINASE PRECURSOR (E UVOMORULIN PRECURSOR (FISB).7 PROTEIN. MHC CLASS II BETA CHAI CHROMOSOME XII COSMID HYPOTHETICAL 43.9 KD CELLODEXTRIN-PHOSPHORY	Description
8.44e-09 3.90e-01 6.36e-00 1.66e+00 1.66e+00 2.67e+00 6.74e+00 6.74e+00 6.74e+01 1.06e+01 1.06e+01 1.06e+01 1.06e+01 1.06e+01	Pred. No.

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PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;

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S GLYCOPROTEIN.	SPIKE PROTEIN.	SPIKE GLYCOPROTEIN.	E2 GLYCOPROTEIN PRECUR	F02E9.6 PROTEIN.	XMN-CADHERIN (FRAGMENT	F56H6.7 PROTEIN.	ABCA (FRAGMENT).	PHOSPHOGLUCOMUTASE A.	12S CRUCIFERIN SEED ST	CAP8E.	CAP5E.	HYPOTHETICAL 36.1 KD P	C-TYPE CYTOCHROME SYNT	HYDROXYMETHYLGLUTARYL-	F35G12.10 PROTEIN.	P2604 PROTEIN (ORF YPL	12S STORAGE PROTEIN (F	S GLYCOPROTEIN.	SURFACE GLYCOPROTEIN S	SURFACE PROTEIN.	PDR5-LIKE ABC TRANSPOR	HYPOTHETICAL 108.0 KD	GUANINE NUCLEOTIDE REG	ABR.
1.66e+01	1.66e+01	1.66e+01	1.66e+01	1.66e+01	1.66e+01	1.66e+01	1.66e+01	1.66e+01		1.66e+01	1.66e+01	1.66e+01	1.66e+01	1.66e+01	1.66e+01	1.66e+01	1.66e+01	1.06e+01	1.06e+01	1.06e+01	1.06e+01	1.06e+01	1.06e+01	1.05e+01

008 E		D AC	ID	8 6 7 7	Qy	밁	Qu Be Ma	SQ	FT	KW	DR	DR !	DR	ဂ္ဂ	RL	₽ ;	200	RP R	g (C	88	SO	GN	DE	ĎΪ	Ţ	Į,	AC.	RESULT
ADHERIN. DACHSOUS. DROSOPHILA MELANOGASTER (FRUIT FLY). EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;	996 (TREMBLREL. 01, 998 (TREMBLREL. 08,	Q24292; 01-NOV-1996 (TREMBLREL. 01, CREATED)	Q24292 PRELIMINARY; PRT; 3380 AA.			81 QKITYRISGVGID 93	Query Match 91.1%; Score 92; DB 11; Length 993; Best Local Similarity 100.0%; Pred. No. 8.44e-09; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	E 993 AA;		CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; CALCIUM-BINDING; REPEAT.		PROSITE; PS00232; CADHERIN; 2.			_	ISHIKAWA H., LI K., UITTO J.;	STRAIN-BALB/C:	SEQUENCE FROM N.A.	SCIURUGNATHI; MURIDAE; MURINAE; MUS.	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;		DSG3.	(FRAGMENT).	(TREMBLREL. 08, LAST	05,	1998 (TREMBLREL.		O35902 PRELIMINARY: PRT: 993 AA.

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RESULT
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FIXBASE; FBgn000497; ds.
PROSITE; PS00233; CADHERIN; 18.
PFPAM; PF00028; cadherin; 26.
CELL ADHESION; GLYCOPROTEIN; TRANS
SEQUENCE 3380 AA; 366356 MW; 7
MEDLINE; 98196666.

DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJ FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; "The complete genome of the hyperthermophilic bacter mardicus.";
NATURE 392:353-358(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       066968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMLIN N., LAWSON D., BARRELL B.;
SUBMITTED (OCT-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AL008970; E1332566; -.
SEQUENCE 2269 AA; 267233 MW; 11E1C8E0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1017
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                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE.
                                                                                                                                                                                                                                                                                                                                                                                            PURM.
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PLASMODIUM
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01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-VF5;
                                                                                                                                                                                                                                                                                                                            BACTERIA;
                                                                                                                                                                                                                                                                                                                               AQUIFEX AEOLICUS.
BACTERIA; AQUIFICALES;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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6.36e-01
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3.90e-01
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                                                                                                                                          AUJAY M.,
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SEQUENCE
STRAIN=CV. COLUMBALL.
A ROUNSLEY S.D., LIN X., KETCOL...
A ROUNSLEY S.D., LIN X., KETCOL...
A SYKES S.M., KAUL S., MASON T.M., KERLAV-L.

RA SOMERVILLE C.R., VENTER J.C.;
RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BAN EMBL; AC003000; G2642153; --

EMBL; AC003674; G2795810; --

TOTENCE 441 AA; 47873 MW; F462C421 CRC32; --

TOTENCE 441 AA; 47873 MW; --

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Best Local S
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01-MAY-1997 (TREMBI
SURFACE PROTEIN PRI
HUMAN CORONAVIRUS.
VIRUSES; SSRNA POSI
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01-JAN-1998 (TREMBLR
01-JUN-1998 (TREMBLR
1517.1 PROTEIN
T517.1 OR F17A14.8
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Q66291;
SEQUENCE FROM N.Arr
STRAIR-HCV-CC43;
KUENKEL F., HERKLER G.;
ARCH. VIROL. 1411:1123-1131(1996)
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STRAIN-CV. COLUMBIA;
ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRA
SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAM
SOMERVILLE C.R., VENTER J.C.;
SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYTLOCHYTES; SERENATOPHYTA; MEGNOLIOPHYTA; EUDICOTYLEDONS; ROSI
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AULT FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V., SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                  VIRUSES; SSRNA
CORONAVIRIDAE;
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                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                  POSITIVE-STRAND CORONAVIRUS.
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58.3%;
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                                                                                                                                                                       VIRUSES,
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SEQUENCE
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01-JUN-1998
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                                                                                                                                                                                                                                                                                 FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A. LATHICRAY R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., C DOUGHERTY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D. PETERSON J., KERLAVAGE A.R., OUACKENBUSH J., SALZBERG S., HANS YAN VUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J., UTTERBACK T., WATTHEY L., MCDONNALD L., ARTHACH P., BOWMAN C., THE CONTRACT TO THE CONTR
   burgdorferi.";
NATURE 390:580-586(1997).
EMBL; AE0001153; G2688429;
TIGR; BB0509; -.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-ATCC 35210 / MEDLINE; 98065943.
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ARCH. VIROL. 1411:1123-1131(1996).
EMBL; Z32768; G475892; -.
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VIRUSES; SSRNA POSITIVE-STRAND
CORONAVIRIDAE; CORONAVIRUS.
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01-NOV-1996 (TREMBLREL, 01
01-MAY-1997 (TREMBLREL: 03
SURFACE PROTEIN PRECURSOR.
                                                                                                                                                                                                                          GARLAND S., FUJII C.,
SMITH H.O., VENTER J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                      Genomic sequence of a Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       995 NVQYRINGIGV 1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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18
1363
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(TREMBLREL. 06, LA
(TREMBLREL. 08, LA
LA 48.7 KD PROTEIN.
                                                                                                                                                                                                                                                              FUJII C., COTTON M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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larity 45.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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8 1363
8 AA; 150835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 AA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.4%;
45.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06, CREATED)
06, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E DISEASE SPIROCHETE)
SPIROCHAETACEAE; BOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
SURFACE PROTE:
L MW; 4510BD9B (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CREATED)
LAST SEQUENCE UPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 57; DI
Pred. No. 1.0
5; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 57;
Pred. No.
5; Misma
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SURFACE PROTEIN.
MW; A2808D88 CRC
                                                                                                                                                                                          disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIRUSES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                              HORST
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1.66e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BORRELIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UPDATE)
                                                                                                                                                                                                                                                                  ROBERTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1363;
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                                                                                                                                                                                          Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLAYTON R.A.,
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                                                                                                                                                                                                                                                              HATCH
                                                                                                                                                                                                                                                                                                                                                                             HANSON M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        GWINN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ξ.
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                                 SORET PRABASA ARA RANGE PRABAS
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Best Local S
Matches
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Best Local s
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LAMPRECHT S., JELANDE.....0(0).

ACTA HORTICULTURAE 0:0-0(0).

EMBL; Y13938; E324688; -.

EMBL; Y13938; E324688; -.

PFAM; PF01307; Plant_vir_prot; 1.

PFAM; PF01307; Plant_vir_prot; 1.
elegans.";
NATURE 368:32-38(1994).
EMBL; Z50177; E1346901;
TENTENCE 287 AA; 324(
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01-NOV-1996
01-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
COLES L.;
                                                                                                                                                                                                                            WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COOPER J., COOLSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTSING J., ELOYD C., MCMURRAY A., MORTIMOR B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGURAN K., WATERSTON R.,
WATERSON A. WEINTROCK T. WILLIAM N., VAUGHAN K., WATERSTON R.,
WATERSON A. WEINTROCK T. WILLIAM N., VAUGHAN K., WATERSTON R.,
WATERSON A. WEINTROCK T. WILLIAM N., VAUGHAN K., WATERSTON R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q20481
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLEREL. 08, LAST ANNOTATION UPDATE)
STRAWBERRY MILD YELLOW EDGE-ASSOCIATED POTEXVIRUS COA
PARTIAL REPLICASE AND ORF2, ORF3, ORF4.
STRAWBERRY MILD YELLOW EDGE-ASSOCIATED VIRUS (SMYEAV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRUSES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278 RNIAYRINNINVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (JUL-1995)
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(TREMBLREL.)
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larity 38.5%;
Conservative
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                             32464 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48741 MW;
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Pred. No. 2.
6; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
3; M
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LAST SEQUENCE UPDATE)
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                             F4C7797C CRC32
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d. No. 2.67e+00;
Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55; DB 14;
No. 4.25e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 108
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CAENORHABDITIS
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Query Match Best Local

Similarity

DB 5; I 6.74e+00;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q15855 PRELIMINARY;
Q15855; Q16194; Q13799;
Q1-NOV-1996 (TREMBLREL: 01, C
01-NOV-1996 (TREMBLREL: 08, L
01-NOV-1998 (TREMBLEEL: 08, L
SEQUENCE OF 333-472 FROM N.A. MEDLINE; 94306394.
BECKER K.F., ATKINSON M.J., R SIEWERT J.R., HOFLER H.; "E-cadherin gene mutations procarcinomas.";
                                                                                                                                                                                                                    RIMM D.L., MCRROW J.S.;
RIMM D.L., MCRROW J.S.;
"Molecular cloning of human
of the cadherin superfamily."
"""" BIOPHYS. RES. COMM
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SEQUENCE
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SEQUENCE FROM N.A.
STRAIN-DSM 1337;
FUCHS K.P., SCHWARZ W.H., STAUDENBAUER W.L.;
SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES
-I- CATALYTIC ACTIVICOSAMINE POLYMERS OF CHITIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 11
Q59326 ,
Q59326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLOSTRIDIUM THERMOCELLUM. BACTERIA; FIRMICUTES; BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CHITINASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE)
(1.4-BETA-POLY-N-ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UVOMORULIN
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PFAM; PF00704; glycosyl_hydro8; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-LIVER
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                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYRFDGVDID 161
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482 AA;
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larity 66.7%;
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                                                                                                                                                                                                                              COMMUN.
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Pred. No. |
1; Misma
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Pred. No. 6.
1; Mismatci
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LAST ANNOTATION UPDATE)
HERIN) (ARC-1/UVOMORULIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                          BECKER I.,
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RESULT AND REAL SOLUTION OF THE BEST OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
PERCL.
SUBMITTED (AUG-1990) ...
-I- SUBCELLULAR LOCATION: TYPE I MEM-
-I- SUBCELLULAR LOCATION: TYPE I MEM-
-I- SUBCELLULAR LOCATION: TYPE I MEM-
-I- STROLB; E1350097; JOINED.
R EMBL; Z78013; E1345595; JOINED.
R EMBL; Z78018; E13445595; JOINED.
PROSITE; PS002327—CADHERIN; 6.
R PROSITE; PS002327—CADHERIN; 6.
CELL ADHESTON; GLYCOPROTEIN; TRANS
CELL ADHESTON; GLYCOPROTEIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
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Best Local Similarity
Matches 7; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 108599; G340185; -.
EMBL; S72492; E136801; -.
EMBL; S72491; E136801; JOINED
EMBL; X52279; G28822; -.
PROSITE; PS00232; CADHERIN; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TT 13
Q19482 PREL
Q19482; Q23218;
Q1-NOV-1996 (TRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY J., COULSON
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON I
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., KIRSTEN J., MORTLMORE B., O'CALLAGHAN M.
PARSONS J., PECKY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEI
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUTENATON R.,
TATTETMEN J., MATERSTON R.,
TATTETMEN J., MATERSTON R.,
TATTETMEN J., WATERSTON R., VAUTENATON R.,
TATTETMEN J., WATERSTON R.,
TATTETMEN 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
01-AUG-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WATSON A., WEINSTOCK:
"2.2 Mb of contiguous
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F15B9.7 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF01049; Cadherin_C_term; 1.
CELL ADHESION; GLYCOPROTEIN; TRANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRIXEN U.H.;
SUBMITTED (MAR-1990)
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
PERCY C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAYNES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RHABDITINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  515 QKITYRI 521
|||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00028; cadherin; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AUG-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23
878 I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RHABDITOIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54:3845-3852(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.5%;
larity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .878
; 96741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
                                                                                                                                                                                                                                                                                                               TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TO EMBL/GENBANK/DDBJ
TION: TYPE I MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   엉
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GENBANK/DDBJ DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01,
07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Œ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 54;
Pred. No.
0; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEMBRANE;
POTENTIAL.
                                 TRANSMEMBRANE; CALCIUM-BINDING; W; 1D187623 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UVOMORULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8F7F0180 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PELODERINAE;
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                                                                                                                                                                                                                                                                                                           DATA BANKS.
PROTEIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DATA BANKS.
PROTEIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RHABDITIA; RHABDITIDA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CALCIUM-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WOHLDMAN
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                                                                                                                                                                                                                                                                                                           SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOHNSTON L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COULSON
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RESULT 14

O77862 PRELIMINARY; PRT; 82 AA.

AC 077862 PREMBEREL. 08, CASTED

OT 01-NOV-1998 (TREMBEREL. 08, LAST SEQUENCE UPDATE)

OT 01-NOV-1998 (TREMBEREL. 08, LAST SEQUENCE UPDATE)

OT 01-NOV-1998 (TREMBEREL. 08, LAST SEQUENCE UPDATE)

OT 01-NOV-1998 (TREMBEREL. 08, LAST SEQUENCE NUTLOTICA).

COMMIC CLASS II B LOCUS 4 (FRAGMENT).

OC CLASKOTA; METAZOA; CHORDATA; VETTEBRATA; ACTINOPTERYGII; NEOPTERYGII;

COMECKARYOTA; METAZOA; CHORDATA; VETTEBRATA; ACTINOPTERYGII; NEOPTERYGII;

COMECKARYOTA; METAZOA; CHORDATA; VETTEBRATA; ACTINOPTERYGII; NEOPTERYGII;

RELAGA-TRILLO E., MCANDREW B., VINCEK V., ZALESKA-RUTCZYNSKA Z.,

RA MALAGA-TRILLO E., MCANDREW B., VINCEK V., ZALESKA-RUTCZYNSKA Z.,

RA SUBLIVMANN H., FIGUEROA F., KLEIN J.;

RI TINAGGE Relationships and Haplotype Polymorphism among Cichlid MHC

CLASS II B genes.";

RI GENETICS 149:1527-1547(1998).

DR MHC.

FT NON_TER 82

SQ SEQUENCE 82 AA; 9607 MW; D1718622 CRC32;
                                                                            Query Match
Best Local S
Matches
   Query Match 52.5%;
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 53.5%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                            NON_TER
NON_TER
SEQUENCE
                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE; 94018589.

ONO H., O'HUIGIN C., TICHY H., KLEIN J.;

"Major-histocompatibility-complex variation
fishes from Lake Malawi.";

MOL. BIOL. EVOL. 10.1060-1072(1993).

EMBL; L17460; G309928; -.

EFRAM; PF00969; MHC_II_beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           O31536 PRELIMINARY; PRT; 82 AA.
O31536; (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
MHC CLASS II BETA CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                     PSSUDOTROPHEUS ZEBRA.
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
TALBOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; F
LABROIDEI; CICHLIDAE; PSEUDOTROPHEUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  612 QKITYRI 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match
Local Similarity 50.0%;
hes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 AQKETYCLNNIGID 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 TOXITYRISGVGID 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 QKITYRI 9
                                                                            1
82
82 AA;
                                                                       82
9754 MW;
   Score 53; DB 7; Len
Pred. No. 1.06e+01;
4; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 53; DB 7; L
Pred. No. 1.06e+01;
4; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 54; DB 5; L
Pred. No. 6.74e+00;
0; Mismatches 0
                                                                            90E5E756 CRC32;
                                                                                                                                                                                                                                                                                                                                        ; ACTINOPTERYGII; NEOPTERYGII; PERCOMORPHA; PERCIFORMES;
                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ω.
                                    Length 82;
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                                                                                                                                                                                                                          two species of cichlid
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   Indels
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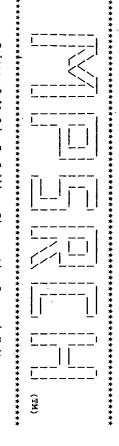
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69 AQKETYCLPNIGID 82
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Length 2610;

Search completed: Fri Jun Job time : 130 secs. 17:11:56 1999



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fr1 Jun 11 17:20:38 1999; MasPar time 4.88 Seconds 65.330 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-991-628-2 (1-15) from US08991628.pep 105

Scoring table:

PAM 150 Gap 15

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
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29:part29 30:part30 31:part31 37:part32 33:part33
34:part24 35:part35 36:part36 37:part37 38:part38

Statistics: Mean 18.438; Variance 59.855; scale 0.308

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

332 1098 1111 1111 1111 1111 1111 1111 1111	Result No.
105 105 105 105 86 88 87 57 57	Score
1100.0 1100.0 1100.0 81.9 81.9 81.9 84.3 54.3 54.3 54.3 54.3 3.3	Query Match
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W04842 W09966 W09968 W09968 R307908 R307942 R93961 R93962 R15489 W113009 W13009 W13009 W13009 W13134 W49731 R49731 R49731 R49731 R49730 R49	Ħ
Self epitope of desmo peptide combining wit pemphigus vulgaris an Human pemphigus vulgaris an Human pemphigus foliaceus a peptide combining wit peptide combining wit pemphigus foliaceus a segment of desmosomal sequence encoded by h Cadherin-11. Sequence encoded by h Sequence encoded by m Full length human cad Human cadherin-11. Human protocadherin p Arabidopsis chloropla	Description
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RESULT	<u></u>
S E	W04842 Standard; peptide; is AA. W04842:
DŢ	18-FEB-1997 (first entry)
DE	Self epitope of desmoglein 3, implicated in autoimmune disease.
?	Tolerisation; self-epitope; antigen; autoimmune disease;
3	autoantigen; HLA; human leukocyte antigen; T-cell; thymocyte;
X X	<pre>pempnigus vulgaris; desmogiein; multiple scierosis; herpes simplex virus; adenovirus; phosphomannomutase;</pre>
KΨ	human papillomavirus; Epstein-Barr virus; DNA polymerase;
ΚW	influenza; haemagglutinin; reovirus; sigma protein.
S	Homo sapiens.
PN	WO9627387-A1.
PD	12-SEP-1996.
ΡF	07-MAR-1996; U03182.
, P	07-MAR-1995; US-400796.
٩: :	Strominger II. Wichbernfennig KW:
DR	42.
PT	Pemphigus vulgaris auto-antigens and multiple sclerosis non-self
3 13	
Α, Ε	auto-immune disease
PS	Claim 1; Page 38; 58pp; English.
S	Pharmaceutical preparations for tolerisation to antigens comprise
ဌ	either an isolated human non-collagen or non-myslin basic protein
S	(MBP) polypeptide which is capable of tolerising an individual to an
ဂ္ဂ	autoantigen; or an isolated human pathogen polypeptide capable of
8	tolerising an individual to that polypeptide. In both cases, the
36	polypeptide (whether sell of non-sell) includes an amino acto
3	protein such as HIA-DR which is Associated with a human autoimmune
င္ပ	disease and which binds to the polypeptide to activate autoreactive
ဌ	T-cells in individuals with the autoimmune disease. This peptide is
င္ပ	derived from the human desmoglein 3 protein (amino acids 97-111)
င္ပ	and is implicated as a self epitope in pemphigus vulgaris. Peptides
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30-JUN-1995; 165632.
30-JUN-1994; JP-17329:
(NISH/) NISHUKAWA T.
WPI; 96-388562/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-interepidermal cellular antibody-combining peptide - which can be immobilised on column to form adsorbent useful for treating diseases related to the antibody Claim 1; Page 2; 7pp; Japanese.

A new peptide is disclosed which contains at least 5 contiguous amino acids from the sequence Val Gly Ile Asp Gln Pro Pro Phe Gly Ile Phe Val Val Asp Lys Asn Thr Gly Asp Ile Asn Ile Thr Ala Ile Val Asp Arg Glu Glu (the present sequence), the peptide not containing more than 50 residues. The peptide combines with anti-interepidermal cellular antibody. It can be immobilised on a carrier to prepare an absorbent useful for the treatment of diseases related to anti-interepidermal
Fused protein recognised by pemphigus vulgaris auto:antibody useful to treat and diagnose pemphis vulgaris (laim 1; Page 7-9; 9pp; Japanese. W07908 represents the human pemphigus vulgaris (PV) antigen extracellular region. The PV antigen is produced in patients wipemphis vulgaris resulting in autoimmune disease. PV is a rare relapsing disease causing suprabasal, intra-epidermal bullae (vesicles) of the skin and mucuous membranes, which is fatal if untreated. The PV antigen was fused to a human IgGl hinge regio and the resulting fusion protein is useful to treat or diagnose Sequence 614 AA;
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Peptide combining with
anti-interepidermal ce
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18-MAY-1994; JP-129556.
(KURS ) KURARAY CO LTD.
WPI; 96-045392/05.
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W07908;
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Autoantibody; immunoglobulin G; IgGl; fusion protein; di
reatment; pemphigus vulgaris; PV; bulla; blister; skin
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1. No. 2.95e-04;
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15-DEC-1992.
27-NOV-1991; 7
27-NOV-1991; 7
                                                                                          diseases related to the antibody

Example 1; Page 4; 7pp; Japanese.

New peptides are disclosed which contain at least 5 contiguous amino acids from the sequence val Gly Ile Asp Gln Pro Pro Phe Gly Ile Phe val Val Asp Lys Asn Thr Gly Asp Ile Asn Ile Thr Ala Ile Val Asp Asp Glu Glu (see R93960), the peptide not containing more than 50 residues. The peptide combines with anti-interepidermal cellular antibody. It can be immobilised on a carrier to prepare an absorbent useful for the treatment of diseases related to anti-interepidermal cellular antibody. The present sequence is a specific example of the new peptides.

Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-1996 (first entry)
Peptide combining with anti-interepidermal cellular antibody.
anti-interepidermal cellular antibody; autoantibody; adsorbent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is the pemphigus vulgaris 130kD antigen. The protein and its encoding DNA may be used in the diagnosis and treatment of pemphigus vulgaris. It is thought that the antigen may be a cell adhesion molecule.

Sequence 999 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding pemphigus vulgaris a diagnostic and therapeutic uses Disclosure; Fig 7; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                             Anti-interepidermal cellular be immobilised on column to f
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keratinocyte cell su
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8-MAY-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                            MAY-1994; 129556.
MAY-1994; JP-129556.
RS ) KURARAY CO LTD.
; 96-045392/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pemphigus vulgaris 130kD antigen:
igus vulgaris; skin disease; autoæntibodies;
inocyte cell surface antigen; glycoprotein;
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15; Conser
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  similarity 100.0%;
12; Conservative
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larity 100.0%;
Conservative
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V, Stanley JR;
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  Score
Pred.
0; M
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re 86; DB 16; Le
1. No. 4.18e-02;
Mismatches 0;
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No. 2.95e-04;
No. 2.95e-04;
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Best Local S
Matches 1
pemphigus foliaceus antigen-IgG constant region fusion protein - lir through the hinge region used to treat pemphigus foliaceus Claim 1; Page 10-12; 17pp; Japanesse.

This sequence represents a fused protein recognised by pemphigus foliaceus patient autoantibody which comprises the constant region of IgG linked to the extracellular region of pemphigus foliaceus antigen protein through the hinge portion. Pemphigus foliaceus is a chronic, generalised, vesicular and scaling skin eruption similar to dermatitis herpetiformis. The pemphigus foliaceus antigen fusion protein is useful to treat pemphigus foliaceus. The antigen is especially administered through an adsorbent upon which the fusion protein is immobilised via a carrier. The fusion protein is also useful for detecting pemphigus foliaceus antibodies which is useful
                                                                                                                                                                                                                                                                J09077800-A.
25-MAR-1997.
12-SEP-1995;
12-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases related to the antibody
Example 2; Page 5; 7pp; Japanese.
New peptides are disclosed which contain at least 5 contiguous amino acids from the sequence Val Gly Ile Asp Gln Pro Pro Phe Gly Ile Phe Val Val Asp Lys Asn Thr Gly Asp Ile Asn Ile Thr Ala Ile Val Asp Arg Glu Glu Glu (see R93960), the peptide not containing more than 50 residues. The peptide combines with anti-interepidermal cellular antibody. It can be immobilised on a carrier to prepare an absorbent useful for the treatment of diseases related to anti-interepidermal cellular antibody. The present sequence is a specific example of the new peptides.
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J07309893-A.
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Pemphigus foliaceus antigen-IgG constant region fusion p

Pemphigus foliaceus; autoantibody; constant region; IgG;

extracellular region; antigen; hinge pertion; skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAY-1994; 129556.
18-MAY-1994; JP-12956.
(KURA) FURARRAY CO LTD.
WPI; 96-045392/05.
Anti-interepidermal cellular antibody-combining peptide - which be immobilised on column to form adsorbent useful for treating
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                                                                                                                                                                                                                                                                                                                                                                                               dermatitis herpetiformis; fusion protein;
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                                                                                                                                                                                                                                                                                                                                                    domain
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18-MAY-1994;
                                                                                                                                                                                                                                   (NISH/) NISHIKAWA T.
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JP-260899.
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llular antibody; autoantibody; adsorben
                                                                                                                                                                                                                                                                                                                                "Pemphigus foliaceus antigen protein"
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Pred. No. 4.18e-02;
"" matches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                  detection; ss.
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R WPI; 97-146518/14.

The Antibody reactive with part of desmosomal cadherin - exposed on surface of epithelial or carcinoma cells, not bound to desmosomes, present for diagnosis and treatment of carcinoma micrometastases PS Claim 7; Page 5; Bpp; German.

CC The present sequence is a segment of the desmosomal cadherin (DC), CC desmoglein Dsg2, which is exposed on the surface of epithelial or carcinoma cells and not bound to desmosomes. An antibody (Ab) CC diagnose, i.e. to detect carcinoma cells, especially CC micrometastases, not bound to desmosomes. An antibody and concett living or fixed carcinoma cells by cell sorting methods and CC das a therapeutic to deliver agents, e.g. other Ab or toxins, to compare the carcinoma, and detects parts of DC that are not compared to the carcinoma, and detects parts of DC that are not compared to the carcinoma cells, as in normal tissue or
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ACCORDED BY RESULT.

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Matches
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Matches 9; Consei
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23-AUG-1995; DE-031033.
23-AUG-1995; DE-031033.
(PROG-) PROGEN BLOTECHNI
(PROG-) PROGEN SCHAEFER S;
                             (FARH ) HOECHST JAPAN I.
Amann E, Kawai S, Oka
WPI; 94-076152/10.
N-PSDB; Q44393.
                                                                                                                                                                    Homo sapiens
EP-585801-A.
09-MAR-1994
25-AUG-1993; 113602.
28-AUG-1992; JP-2300
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R49732
R49732
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Sequence 778 AA;
                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-1994 (first entry)
Sequence encoded by human
OSF-4-2; cadherin; growth
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DE19531033-A1.
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cadherin; desmoglein; Dsg2; cell; surface; epithe
cadherin; desmoglein; Dsg2; cell; surface; epithe
desmosome; antibody; epitope; diagnosis; detectio
desmosome; antibody; epitope; diagnosis; detectio
tasis; separation; enrichment; targetted delivery;
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   cadherin-like
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                                                                                                      AN LTD.
Okazaki
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factor;
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Pred.
5; M
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Pred.
5; M
   OSE-4
                                                                                                          Takeshita
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No. 6.96e-02;
                                                                                                                                                                                                                                                                                                                                                                                     cDNA.
osteogenesis;
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1.16e-01;
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                                                                                                      Tsujimura
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                                                                                                                                                                                                                                                                                                                                                                                        osteoblast;
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C line MC3T3-El and from mouse liver tissue, amplified by PCR, and
C then as much common DNA as possible removed by hybridisation between
C the 2 libraties. Residual El-specific DNA was amplified, inserted
C into lambda gtl0 and screened by plaque hybridisation. A minibank of
C 273 E-specific clones was recovered, their inserts amplified and
C used to screen total RNA from both cell types. One clone specific
C for El was identified and sequenced. The insert from this clone was
C used to screen cDNA prepd. from El RNA and the longest posn. insert
C cloned in pGEM 112f (+) to give pKOT164. This insert was sequenced;
it encoded the 796 AA mouse precursor protein (Q44391/R49730). The
C insert was also used to screen a cDNA bank prepd. from human
CC osteosarcoma to identify 2 clones encoding the 2 human precursor
CC proteins - OSF-4-1 and OSF-4-2 (Q44392/R49731 and Q44393/R49732
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                                                                    Query Match
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The likelihood of establishing and maintaining a pregnancy, blastocyst implantation or endometrial receptivity are determined by measuring the level of cadherin-11 mrNA or protein in endometrial cells. A level below a standard value indicates inability to establish or maintain pregnancy. Women who are identified as having low level expression of cadherin-11 in endometrial cells can then be treated with a genetic construct comprising the cadherin-11 cDNA. The expression of cadherin-11 from the construct increases fertility and lessens the likelihood of miscarriage.

Cadherin-11 expression is a better predictor of endometrial response and receptiveness than conventional analysis of endometrial cell
                                                                                                                                                                                                                                                                                                                                                                                                 Assessing likelihood of successful pregnancy by measuring levels cadherin-11 in endometrium - also diagnosis of infertility from 1 cadherin levels and increasing cadherin levels by administering progestin or cadherin-encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; V83124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maccalman CD, Step WPI; 99-024071/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-APR-1997; CA-203718.
(UYBR-) UNIV BRITISH COLUMBIA.
MACCALMAN CD, Stephenson MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cadherin; morphogenisis; calcium-dependent cell adhesion; pregnancy; endometrium; trophoblast; balstocyst; infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W85598 standard; protein; 796
W85598;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
WO9849560-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cadherin-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and diagnosis of bone metabolic disease, and nucleic acid encoding them encoding them Claim 1; Page 23-27; 34pp; English.

CDNA libraries were constructed from the mouse osteoblast:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAR-1999 (first entry)
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larity 50.0%;
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larity 50.0%;
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Pred. No.
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Pred. No. 5.11e+01;
5; Mismatches 1
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                                                                    Mismatches
                                                                                     DB 38;
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09-MAR-1994.
25-AUG-1993;
28-AUG-1992;
then as much common DNA as possible removed by hybridisation between the 2 libraries _Besidual E1-specific DNA was amplified, inserted into lambda gtt0 and screened by plaque hybridisation. A minibank of 273 E-specific clones was recovered, their inserts amplified and used to screen total RNA from both cell types. One clone specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-SEP-1994 (first entry)
Sequence encoded by murine OSF-4 cDNA.
OSF-4; cadherin; growth factor; osteogenesis; osteoblast; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273 E-specific clones was recovered, their inserts amplified and used to screen total RNA from both cell types. One clone specific for El was identified and sequenced. The insert from this clone was used to screen cDNA prepd. from El RNA and the longest posn. insert cloned in pGEM 112f (+) to give pKOT164. This insert was sequenced; it encoded the 796 AA mouse precursor protein (Q44391/R49730). The insert was also used to screen a cDNA bank prepd. from human osteosarcoma to identify 2 clones encoding the 2 human precursor proteins. OSF-4-1 and OSF-4-2 (Q44392/R49731 and Q44393/R49732
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CDNA libraries were constructed from the mouse osteoblastic cell

line MC3T3-El and from mouse liver tissue, amplified by PCR, and
then as much common DNA as possible removed by hybridisation between
the 2 libraries. Residual El-specific DNA was amplified, inserted
into lambda gt10 and screened by plaque hybridisation. A minibank of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New bone related, cadh and diagnosis of bone encoding them Claim 1; Page 18-22; 3
                                                                                                                               encoding them Claim 1; Page 13-17; 34pp; English. Claim 1; Page 13-17; 34pp; English. CDNA libraries were constructed from the mouse osteoblastic cell line MC3T3-E1 and from mouse liver tissue, amplified by PCR, and
                                                                                                                                                                                                                                                New bone related, cadherin-like OSF-4 proteins - for and diagnosis of bone metabolic disease, and nucleic
                                                                                                                                                                                                                                                                                                                         28-AUG-1992; JP-230028.
(FARH ) HOECHST JAPAN LTD.
Amann E, Kawai S, Okazaki
WPI; 94-076152/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus.
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Amann E, Kawai S, Okazal
WPI; 94-076152/10.
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R49731;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAR-1994.
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28-AUG-1992;
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796 AA;
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oone metabolic
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17-APR-1992; US-872643.
19-APR-1993; US-049460.
26-JAN-1994; US-188228.
(DOHE-) DOHENY EYE INST.
                        08-JUL-1997.
17-APR-1992;
19-APR-1993;
17-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is full length human cadherin-11, which is a Ca2+ dependent cell adhesion protein. The human cadherin cDNA using probes based on homologous rat cadherin cDNA ibrary, using probes based on homologous rat cadherin cDNA. Antibodies or fragments that specifically bind the human cadherin can be used to purify the cadherin, determine its tissue expressicant antagonise its ligand/antiligand binding activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for El was identified and sequenced. The insert from this clone was used to screen cDNA prepd. from El RNA and the longest posn. insert cloned in pGEM 112f (+) to give pKOT164. This insert was sequenced; it encoded the 796 AA mouse precursor protein (944391/49730). The insert was also used to screen a cDNA bank prepd. from human osteosarcoma to identify 2 clones encoding the 2 human precursor proteins - OSF-4-1 and OSF-4-2 (944392/R49731 and 944393/R49732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Full length human cadherin-11.
Ca2+ dependent; cell adhesion protein; foetal; cadherin; rat;
brain; human; antibody; purification; determination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              respectively).
Sequence 796 AA;
                                                                                                                                                                                                                                                                                 W25636;
W25636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                           Human cadherin: 11.

Human; cadherin; rat; calcium-dependent cell adhesion superfamily; cytoskeleton; eatenin; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Columns 95-100; 59pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; T6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suzuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W13134 standard;
                                                                                                                             US5646250-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JAN-1997
                                                                                                                                                                                                                                                           03-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100
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uence .796
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                                                                                                                                                                                                                                                                                                                                                                                                                    IFVVDKNTGDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ifviddksgnih 111
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)B; T61925.
                                                                                                                                                                                                                                                                                                           standard; Protein; 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; antibody; purification; determine expression; binding antagonist; calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
872643.
US-049460.
US-872643.
US-332638.
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larity 50.0%;
Conservative
                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cadherin proteins -
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                                                                                                                                                                                                                                                                                                                                                                                                                    14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       796 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 57;
Pred. No.
5; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
                                                                                                                                                                                                                                                                                                              A
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No. 5.11e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful as cadherin antagonists,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21;
5.11e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ۲.
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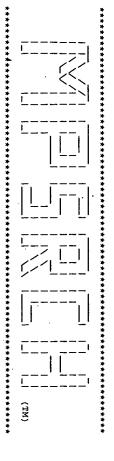
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ΩV
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                                                                            Polynucleotide(s) encoding human protocadherins pc3 and pc4 and rat pc5 - involved in cell-cell adhesion and regulation activities claim 16; Page 122-125; 146pp; English.

Claim 16; Page 122-125; 146pp; English.

C R86865-R86867 represent the sequences for three protocadherins. This sequence represents the human protocadherin pc4. These sequences are related to cadherin, and possess cell adhesive ability. Cadherins are glycosylated integral membrane proteins that are involved in cell-cell adhesion. Cadherins are composed of an N-terminal extracellular domain which consists of 5 unique subdomains, a membrane spanning domain, and a cc-terminal cytoplasmic domain. The cytoplasmic domain interacts with the cytoplasmic domain is not present in all cadherins, but in those which possess it, it is essential for the cadherins, but in those which possess it, it is essential for the cadherins adhesive function. The cadherins which do not possess a cytoplasmic domain appear to function via a different method from those with a cytoplasmic domain.

These sequences were isolated using primers 1 and 2 (see T03575 and the cell-cell adhesive properties. Antibodies produced against these composes are useful for mediation activity of these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local s
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cadherin-8, -5, -11 and -13. Cadherins are calcium-dependent cell adhesion proteins. They are glycosylated integral membrane proteins that have an N-terminal extracellular domain that determines binding specificity, a hydrophobic membrane spanning region and a C-terminal cytoplasmic domain, which is highly conserved among members of the superfamily. The C-terminal domain interacts with the cytoskeleton through eatenins and other cytoskeleton-associated proteins. The novel cadherin proteins may be used in the analysis of the role of cadherins in various cancers. Sequence analysis of the cadherin proteins also allows investigation of the structure and function of cadherin. The cadherin proteins may be isolated by using anti-cadherin antibodies. These antibodies may also be used to modulate the activity of cadherins. Each subclass of cadherins has a unique tissue distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human and rat cadherin
Claim 1; Column 89-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents human cadherin-1 provides details of human cadherin-5, -8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suzuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 96-068873/07.
N-PSDB; T03573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human protocadherin Protocadherin; pc3;
   protocadherins,
Sequence 797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  catenin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DOHE-)
                                                          sequences are useful for modulating the binding activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-1995; U08071.
27-JUN-1994; US-268161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
WO9600289-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R86866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R86866 standard; Protein; 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOHE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 ifviddksgnih 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOHENY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          796 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EYE
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   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INST
                              can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pc4; pc5; human; rat; cadherin; cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide(s) - 56pp; English.
                                 e
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human cadherin-11. To the following the
                              used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
5; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               re 57; DB 23; I
d. No. 5.11e+01;
Mismatches 1;
                              therapeutically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mediate cell-cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                he invention specifically -12 and -13, and rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
```

<pre>Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0; Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0; 288 fqpfvideitgeihl 302</pre>
7; Conservative 4; Mismatches 4; Indels 0; Gaps 0; qpfvideitgeihl 302 : : : : : :
Conservative 4; Mismatches 4; Indels 0; Gaps 0; eitgeihl 302 : :: : :
46.7%; Pred. No. 5.11e+01; vative 4; Mismatches 4; Indels 0; Gaps 0; 1 302 ; 1 15
4; Mismatches 4; Indels 0; Gaps 0;
Mismatches 4; Indels 0; Gaps 0;
nes 4; Indels 0; Gaps 0;
; Indels 0; Gaps 0;
Indels 0; Gaps 0;
0; Gaps 0;
Gaps 0;
0,



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:18:54 1999; MasPar time 4.32 Seconds 139.098 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-991-628-2 (1-15) from US08991628.pep 105 1 FGIFVVDKNTGDINI 15

Scoring table: PAM 150 Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

Mean 26.793;

Variance 39.116; scale 0.685

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

110 110 110 110 110 110 110 110 110 110	Result
1321000876554432 13210008765554432 10008776555555555555555555555555555555555	. Score
100.0 80.0 78.1 78.1 62.9 62.9 61.9 61.9 61.9 58.1 57.1 57.1 55.2 55.2 55.2 55.2	Query
1043 11043 11043 11117 11117 1785 785 839 779 824 1626 1626 1626 1798 1798 1798 1798 1798 1798 1798 1798	Length I
444040000000000000000000000000000000000	DB E
IJHUG3 IJHUG3 IJHUG3 IJHUG3 IJHUG1 IJHUG3 IJ	ID
desmoglein 3 precurso desmoglein 1 precurso desmoglein 2 - human desmoglein 2 - human desmocollin 1a - bovi cadherin 7 - chicken desmocollin 1b precur Dscla precursor - hum DNA topoisomerase (AT hypothetical 10.6 kD hypothetical protein aldehyde ferredoxin o camberin 14 - human conserved hypothetical protein protein - cucurb conserved hypothetical BH-protocadherin PCDH BH-protocadherin PCDH	Description
1.59e-09 6.33e-05 6.33e-05 6.33e-05 6.37e-01 2.45e-01 2.45e-01 3.76e-01 3.76e-01 3.76e-01 3.76e-01 3.76e-01 3.76e-01 3.76e-01 3.76e-01 3.76e-01 4.53e+00 4.53e+00 6.75e+00 6.75e+00	Pred. No.

45	44	3	42	41	40	39	38 8	37	36	35 5	34	ω ω	32	<u>ы</u>	30	29	28	27	26	25	
55	ភូ	55	55	55	55	55	55	56	56	57	57	57	57	57	57	57	57	57	57	58	
52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	53.3	53.3	54.3	54.3	54.3	54.3	54.3	54.3	54.3	54.3	54.3	54.3	55.2	
1827	1827	1615	1196	884	790	211	112	756	713	1400	887	798	796	796	796	796	504	209	209	3027	1
Ь	ᆫ	ب	N	<u>-</u>	N	N	N	N	N	N	Н	N	Ņ	ผ	N	N	Н	N	N	N	
A23945	DHUU	TRMINW	S46430	IJMSCE	I50178	F69391	D64455	S67433	B38992	138185	IJCHCL	S62791	A53584	149556	A38992	148277	G71248	F71830	C64685	JQ1917	
sucrose alpha-glucosi	sucrose alpha-glucosi	180K protein - tomato	botulinum neurotoxin-	E-cadherin precursor,	cadherin-6B - chicken	hypothetical protein	hypothetical protein	hypothetical protein	cadherin 13 precursor	protein-tyrosine kina	E-cadherin precursor,	.probable lipoprotein	OB-cadherin precursor	cadherin-11 - mouse	cadherin 11 precursor	cadherin-11 - mouse	tldD homolog PH0246 -	ribonuclease hii - He	ribonuclease HII - He	polyprotein - parsnip	
2.18e+01	2.18e+01	2.18e+01	2.18e+01	2.18e+01	2.18e+01	2.18e+01	2.18e+01	1.48e+01	1.48e+01	1.00e+01	1.00e+01	1.00e+01	1.00e+01	1.00e+01	1.00e+01	1.00e+01	1.00e+01	1.00e+01	1.00e+01	6.75e+00	

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Query Match Best Local Sim Matches 15;	910-938 937-966 110,180,545 SUMMARY	50-615 52-157 160-267 270-383 390-495 496-598 616-639	FEATURE 1-23 24-49 50-999	GENETICS #gene #gene #cross-re #map_position CLASSIFICATION KEYWORDS	#title Autorial Autor	RESULT 1 ENTRY TITLE ALTERNATE NAMES ORGANISM DATE ACCESSIONS REFERENCE #AUTHORS #Journal
1 100.0%; Score 105; DB 1; Length 999; Similarity 100.0%; Pred. No. 1.59e-09; 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	#domain desmoglein repeat #label DGN #domain desmoglein repeat #label DGN #binding_site carbohydrate (Asn) (covalent) #status predicted #length 999 #molecular-weight 107502 #checksum 8311	extracellular *status procedherin repeat homology cadherin repeat homology transmembrane *status protection repeat homology transmembrane *status protection repeat homology transmembrane *status protection repeat *status protectio	transmembrane protein #domain signal sequence #status predicted #label SIG\ #domain propeptide #status predicted #label PRO\ #product desmoglein homolog #status predicted #label MAT\	GDB:DSG3 ferences GDB:134030; 18q12.1-18q12.2 #superfamily cadher calcium binding; ce	tle Autoantibodies against a novel epithelial cadherin in pemphigus vulgaris, a disease of cell adhesion. oss-references MUD:92069753 cession A41088 ##molecule_type mRNA ##residues 1-999 ##label AMA ##cross-references GB:M76482; NID:g190751; PID:g190752	IJHUG3 #type complete desmoglein 3 precursor - human pemphigus vulgaris antigen #formal_name Homo sapiens #common_name man 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 18-Sep-1998 A41088 A41088 A41088 AA1088

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#journal Biochem. Biophys. Res. Commun. (1990) 173:1224-1230
#title Desmoglein shows extensive homology to the cadherin family
cell adhesion molecules.

#cross-references MUID:91097353
#accession A37785
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#title Complete amino acid sequence of the epidermal desmoglein
precursor polypeptide and identification of a second t;
of desmoglein gene.
#cross-references MUID:92037656
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##cross-references GB:S64268; GB:S64270
NCE A37785
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##cross-references GB:X57784
##note this sequence has been revised
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desmoglein 1 precursor - bovine
desmoglein BDCM
#formal_name Bos primigenius taurus #common_name cattle
30-'un-1993 #sequence_revision 30-'un-1993 #text_change
05-Sep-1997
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#superfamily cadherin; cadherin repeat homology
calcium binding; cell adhesion; duplication; glycoprotein;
                                                                                                                                                                                                                                                                       Zimbelmann, R.; Franke, W.W.
Eur. J. Cell Biol. (1990) 53:1-12
Identification of desmoglein, a constitutive desmosomal glycoprotein, as a member of the cadherin family of cell
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Proc. Natl. Acad. Sci. U.S.A. (1991) 88:4796-4800

Desmosomal glycoprotein DGI, a component of intercellular desmosome junctions, is related to the cadherin family cell adhesion molecules.

cell adhesion molecules.
#journal
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Structural analysis and expression
cadherin-like component of the de
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#formal_name Homo sapiens #common_name man
30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
Wheeler, G.N.; Buxton, R.S.; Parker, A.E.; Rees, D.A.; King, I.A.; Magee, A.I. Biochem. Soc. Trans. (1991) 19:1060-1064 Desmosomal glycoproteins I, II and III: no.
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#map_position 18q12.1-18q12.2
CLASSIFICATION #superfamily cadherin; cadherin
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Best Local Similarity
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50-548
                                                                                          #title Complete amino acid sequence of the epidermal desmoglei precursor polypeptide and identification of a second of desmoglein gene.

#cross-references MUID:92037656
#accession B38872
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#cross-references MUID:92175187
#accession A61279
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                                                   ##molecule_type mRNA
##residues 777-1117 ##label
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##residues 1-55 ##label WH3
                                    ##cross-references GB:S64273
                                                                                                                                                                                                                                                                      ##residues 1-1117 ##label ZIM 1-1117 ##cross-references EMBL:226317; NID:g416177; PID:g416178
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#domain desmoglein repeat #label DG3\
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#domain desmoglein repeat #label DG4\
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#domain cadherin repeat homology #label CR3\
#domain cadherin repeat homology #label CR4\
#region serine/threonine-rich\
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Pred. No. 6.33e-05;
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#map_position 18412.1-18412.2
CLASSIFICATION #superfamily cadherin; cadherin
KEYWORDS calcium binding; cell adhesion;
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161-271
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#title
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#title Cloning and sequence analysis of desmosomal glycoproteins and 3 (desmocollins): cadherin-like desmosomal adhesion molecules with heterogeneous cytoplasmic domains.
#cross-references MIID:91185414
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##cross-references EMBL:X56967;
ENCE A60714
                                                                                                        ##molecule_type protein
##residues 1-6,'A',8-9,'R',11-17,'RCE'
##experimental_source nasal epidermis
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1-32;65-76;148-159;164-176;190-205;208-219;238-256;
##residues 361-375;377-388;478-486 ##label KO2
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J. Cell Sci. (1990) 97:339-246
Desmosomal glycoproteins 2 and 3 (desmocollins) show N-terminal similarity to calcium-dependent cell-cell
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Differentiation (1991) 47:29-36
Amino acid sequence of bovine muzzle epithelial desmocollin
derived from cloned cDNA: a novel subtype of desmosomal
#superfamily cadherin; cadherin repeat homology alternative splicing; calcium binding; cell adhesion; duplication; glycoprotein; phosphoprotein; transmem
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#length 1117
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#domain cadherin repeat homology #label CR2
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NID:g310; PID:g311
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duplication; glycoprotein;
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#journal Development (1995) 121:1321-1332
#title Neural crest cell cell adhesion controlled by sequential and
#totss-references.wold:95309115
#cross-references.wold:95309115
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##cross-references GB:D42150; NID:g868000; PID:g868001
##cross-references GB:D42150; NID:g868000; PID:g868001
##crosidues 1-785 #molecular-weight 87171 #chec
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desmocollin 1b precursor - bovine desmosomal glycoprotein 3 #formal_name Bos primigenius taurus #common_name cattle 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 24-Oct-1997 B38456; A39377; S14567
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cadherin-7 - chicken
#formal_name Gailus gallus #common_name chicken
21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
09-May-1997
                                                                                                                                                                                                                                                                 62.9%;
larity 61.5%;
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#molecular-weight 85170
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Pred. No. 2.45e-01;
4; Mismatches 1;
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##cross-references GB:M67489; GB:M61750; NID:g162970; PID:g162971
##note part of this sequence, including the amino end of the
mature protein, was confirmed by protein sequencing
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##cross-references GB:X56966; NID:g315; PID:g316
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Local Similarity 53.8%;
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                                      15-Aug-1997 #sequence_revision B48910
                                                                                       B48910 #type fragment
desmocollin 1b precursor - human (fragment)
#formal_name Homo sapiens #common_name man
08-Dec-1995 #sequence_revision 08-Dec-1995
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J. Cell Biol. (1991) 113:381-391
Cloning and sequence analysis of desmosomal glycoproteins and 3 (desmocollins): cadherin-like desmosomal adhesion molecules with heterogeneous cytoplasmic domains.
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alternative splicing; calcium binding; cell adhesion;
duplication; glycoprotein; phosphoprotein; transmembrane
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#binding_site phosphate (Ser)
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#product desmocollin 1b #status experimental #label MAT\
#domain extracellular #status predicted #label EXT\
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Pred. No. 2.45e-01
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N.K.;
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#title Cloning of the cDNA (DSC1) coding for human type
desmocollin and its assignment to chromosome 18
#cross-references MUID:94116981
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#accession A48910
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##molecule_type mRNA
##residues 1-770 ##label
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Similarity 53.8%;
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#superfamily cadherin; cadherin repeat homology
alternative splicing; calcium binding; cell adhesion;
glycoprotein; phosphoprotein; transmembrane protein
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alternative splicing; calcium binding; cell adhesion;
glycoprotein; phosphoprotein; transmembrane protein
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Cloning of the cDNA (DSCI) coding for human type 1 desmocollin and its assignment to chromosome 18.
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137281 #type complete
Dsc1a precursor - human
#formal_name Homo sapiens #common_name man
12-Aug-1996 #sequence_revision 12-Aug-1996
16-Feb-1997
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#length 770 #checksum 4861
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Best Local Similarity 53.8%;
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#journal Int. J. Dev. Biol. (1993) 37:101-110
#title Differential synthesis of type 1 and
in human stratified epithelia.
#cross-references MUID:93283249
#accession 137282
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#journal Int. J. Dev. Biol. (1993) 37:101-110
#title Differential synthesis of type 1 and
in human stratified epithelia.
#cross-references MUID:93283249
#accession 137281
#authors Dereuddre, S.; Frey, S.; Delaporte, C.; Jacquemin-Sablon, #journal Biochim. Biophys. Acta (1995) 1264:178-182
#title Cloning and characterization of full-length cDNAs coding in the DNA topoisomerase II beta from Chinese hamster lung cells sensitive and resistant to 9-OH-ellipticine.
#cross-references MUID:96085121
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IFICATION #superfamily cadherin; cadherin repeat homolo
RY #length 840 #molecular-weight 93848 #checks
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##molecule_type mRNA
##residues 1-894 ##label RES
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Local Similarity 53.8%;
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                                                                                                                                                                             S59969 #type complete
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) isoform
beta - Chinese hamster
DNA topoisomerase II isoform beta; DNA-gyrase
#formal_name Cricetulus griseus #common_name Chinese hamster
15-Feb-1996 #sequence_revision 13-Mar-1997 #text_change
17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #superfamily cadherin; cadherin repeat homology
#length 894 #molecular-weight 100044 #checksum
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#formal_name Homo sapiens #common_name man
12-Aug-1996 #sequence_revision 12-Aug-1996
16-Feb-1997
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Pred. No. 3.76e-01;
Mismatches 2;
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Pred. No. 3.76e-01
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#authors
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Best Local Similarity 72.7%;
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#Journal Nucleic Acids Res. (1992) 20:5587-5592

#title Isolation of cDNA clones encoding the beta isozyme of human DNA topoisomerase II and localisation of the gene to chromosome 3p24.

#cross-references MUID:93087165

#accession $26730
                                                                                                                                                                                                                                   #authors Austin, C.A.: Fisher, L.M.
#journal FEBS Lett. (1990) 266:115-117
#title Isolation and characterization
a novel DNA topoisomerase II
#cross-references MUID:90306333
#accession S10710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors Chung, T.D.Y.; Drake, F.H.; Tan, K.B.; Per, S.R.; Crooke, S.T.; Mirabelli, C.K.

#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:9431-9435

#title Characterization and immunological identification of cDNA clones encoding two human DNA topoisomerase II isozymes.

#cross-references_MUID:90083281
                                                                     #journal #title
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#cross-references
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NCE A39242
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##cross-references EMBL:X86455; NID:g790987; PID:g790988
##exper1mental_source lung
                                                                                                                                                                ##residues 1043-1276 ##label AUS 10538324; PID:g38325
                                                                                                                                                                                                                 ##molecule_type mRNA
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DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) beta,
splice form 2 · human
DNA topoisomerase II isoform beta-2
DNA topoisomerase II isoform beta-1
#formal_name Homo sapiens #common_name man
04-Oct-1991 #sequence_revision 03-May-1996 #text_change
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DNA topoisomerase (ATP-hydrolyzing) medium chain homology
ATP; DNA binding; DNA replication; isomerase; nucleus
                                      Austin, C.A.; Sng, J.H.; Patel, S.; Fisher, L.M. Biochim. Biophys. Acta (1993) 1172:283-291 Novel HeLa topoisomerase II is the II-beta isoform: complete coding sequence and homology with other type II
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MUID:93192319
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    medium chain homology #label TOP
jth 1612 #molecular-weight 182074 #checksum 5332
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es EMBL:X68060; NID:g37230; PID:g37231
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Pred. No. 2.01e+00;
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KEYWORDS
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REFERENCE
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#map_position 3p24-3p24
CLASSIFICATION #superfamily eukaryotic type II
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GENETICS
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##molecule_type mRNA

##rosidues 596-1430,'S',1432-1610,'A',1612-1626 ##label AU1

##cross-references EMBL:215115; NID:g288564; PID:g288565
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#title
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#journal Nucleic Acids Res. (1993) 21:3719-3723
#title Human cells express two differentially
topoisomerase II-beta mRNA.
#cross-references MUID:93376494
#accession S41641
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                                                                                                                                                                      #accession
                                                                                                                                                                                          #title The complete genome sequence of #cross-references MUID:97426617
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##residues 24-80 ##label DAV
##cross-references EMBL:X71911
##note this sequence represents a
designated beta-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type mRNA
#*residues 1-23,29-1610,'A',1612-1626 ##label AU2
                                      ##residues 1-94 ##label BLAT
##cross-references GB:AE000421; GB:U00096;
UWGP:b3446
                                                                                   ##molecule_type DNA
##residues 1-9
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                 ##experimental_source
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Similarity 72.7%;
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DNA topoisomerase (ATP-hydrolyzing) medium chain homology
alternative splicing; ATP; dimer; isomerase; nucleus
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hypothetical 10.6 KD protein in gntR-ggt in
Escherichia coli (strain K-12)
#formal_name Escherichia coli
12-Sep-1997 #sequence_revision 17-Sep-1997
14-Nov-1997
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                                                                                                                                                                                                                                  Science (1997) 277:1453-1462
                                                                                                                                                                                                                                                                      Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shav
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    medium chain homology #label TOP
jth 1626 #molecular-weight 183296 #checksum 3565
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                                                                                                                                               preliminary; nucleic acid sequence
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                                                                                                                           translation not shown
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Pred. No. 2.01e+00
                    K-12,
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                 substrain
                                                            NID:g1789854; PID:g1789855;
                                                                                                                                                                                                                Escherichia coli K-12
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                                                                   Ouery Match 57.1%;
Best Local Similarity 42.9%;
Matches 6; Conservative
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Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                Yasuda, M.; Tabata, S.

#Journal DNA Res. (1996) 3:109-136

Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein coding regions.
                                                                                                                                                         59 FIIDKDSGEIH 69
|::||::|::
4 FVVDKNTGDIN 14
                               49 FGVLMIDPSTGEIS 62
| | ::::| :||:|:
1 FGIFVVDKNTGDIN 14
                                                                                                                                                                                                                                                                                   S76379
                                                                                                                                                                                                                                                                                                                                                                                                                   Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S76379 #type complete
hypothetical protein - Synechocystis sp. (strain PCC 6803)
#formal_name Synechocystis sp.
PCC 6803
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#length 94 #molecular-weight 10613 #checksum 4152
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Pred. No. 3.02e+00;
7; Mismatches 1
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Search completed: Fri Jun 11 17:20:20 1999 Job time: 86 secs.

****	(MX)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:16:04 1999; MasPar time 2.46 Seconds 172.535 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-08-991-628-2 (1-15) from US08991628.pep 105 1 FGIFVVDKNTGDINI 15

Scoring table:

Sequence:

PAM 150 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot37 1:swissprot

Statistics: Mean 27.494; Variance 34.835; scale 0.789

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 3 3 3 4 4 4 4 4 7 7 7 11 11 11 11 11 11 11 11 11 11 11	Result
105 844 556611 556611 556611 556611 556611	Score
100.0 80.0 80.0 78.1 78.1 58.1 58.1 58.1 57.1 57.1 57.1 57.3 54.3 53.3 53.3 53.3	Query Match
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EMBL; M76482; G190752; -.
PIR; A41088; IJHUG3.
MIN; 169615; -.
PROSITE; PS00232; CADHERIN; 3.
PRAM; PF00028; cadherin; 4.
HSSP; P09803; 1EDH.

or send an email to license@isb-sib.ch).

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ALIGNMENTS

RESULT ID D	LT 1 DSG3_HUMAN STANDARD; PRT; 999 AA.
를 A	P32926; 01-OCT-1993 (REL. 27, CREATED)
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Ä	~
E	GLEIN 3 PRECURSOR
GN	
S	
გ	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
გ	PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN	[1]
RP	SEQUENCE FROM N.A.
2	MEDLINE; 92069753.
RA	
7.T	"Autoantibodies against a novel epithelial cadherin in pemphigus
RI	vulgaris, a disease of cell adhesion.";
2 5	E 6/:869-8//(E99E).
38	INVOLVED IN THE INTERACTION OF PLACES PROTEINS AND INTERMEDIATE
გ	
റ്റ	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ဂ	-!- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL, OESOPHAGUS AND
င္ပ	CARCINOMAS.
ဥ	-!- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
င္ပ	
င္ပ	: PEMPHIGUS VULGARIS (PV) IS A POTENTIALLY LETHAL S
38	DISEASE IN WHICH EPIDERWAL BLISTERS OCCUR AS THE RESULT OF THE
3 6	AGAINST DSG3
2 (CHARLE STREET STREET AND AND CARREST STREET
88	-!- SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS TO THE DESMOSOMAL SUBFAMILY.
င္ပ	
ဂ	This SWISS-PROT entry is copyright. It is produced through a collaboration
გ	between the Swiss Institute of Bioinformatics and the EMBL outstation -
ဂ္ဂ	the European Bioinformatics Institute. There are no restrictions on its
ဂ	use by non-profit institutions as long as its content is in no way
38	modified and this statement is not removed. Usage by and for commercial
36	on and an amil to ligamendacheath and anti-//www.top orbitalists afficement (see nicp.//www.top orbitalists and orbitalists)

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Query Match
Best Local
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CARBOHYD
CARBOHYD
SEQUENCE
SEQUENCE OF 44-493 FROM N.A.

MEDLINE; 91097553.

GOODWIN L., HILL J.E., RAYNOR K., RASZI L., MANABE N
GOODWIN L., HILL J.E., RAYNOR K., RASZI L., MANABE N
PDESMOGICEL SHOWS EXTENSIVE homology to the cadherin
adhesion molecules.";
BIOCHEM. BIOPHYS. RES. COMMUN. 173:1224-1230(1990).
BIOCHEM. BIOPHYS. RES. COMMUN. 173:1224-1230(1990).
-I- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME:
INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS /
FILAMENTS MEDIATING CELL-CELL ADHESION.
                                                                                                               MEDLINE; 9203
KOCH P.J., GO
FRANKE W.W.;
                                                                                                                                                                                                                                                                                           DSG1.
BOS TAURUS (BOVINE).
TOTARYOTA; METAZOA;
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REPEAT
CAREOHYD
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TRANSMEM
DOMAIN
                                                                                                                                                        ZIMBELMANN R., FRANKE W.W.;
"Identification of desmoglein,
glycoprotein, as a member of tl
molecules.",
EUR. J. CELL BIOL. 53:1-12(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
PROPEP
                                                                                                                                                                                                          SEQUENCE OF 44-1043 FROM N.A. TISSUE-MUZZLE EPITHELIUM; MEDLINE; 91168965.
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-MUZZLE EPITHELIUM;
KOCH P.J., GOLDSCHMIDT M.D.,
SUBMITTED (MAR-1991) TO EMBL,
                                                                                                                                                                                                                                                                                                                        01-OCT-1993 (REL. 27, C
01-OCT-1993 (REL. 27, I
01-NOV-1997 (REL. 35, I
DESMOGLEIN 1 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                           DSG1_BOVIN
Q03763;
                                                                                     "Complete amino acid sequence of the epidermal desmoglein precursor polypeptide and identification of a second type of desmoglein gene."; poly. J. CELL BIOL. 55:200-208(1991).
                                                                                                                                                                                                                                                                                       ARTIODACTYLA;
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                                                                                                                                        REVISIONS, AND SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     97
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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Similarity 100.0%;
15; Conservative
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ANTIA; PECORA; BOVOIDEA; BOVIDAE;
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LAST ANNOTATION UPDATE)
R (DESMOSOMAL GLYCOPROTEIN I)
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                                                                                                                        ж. D.,
                                                                                                                                                                                                   SCHMELZ M.,
                                                                                                                                        OF 101-123
                                                                                                                                                                                                                                             4.D., ZIMBELMANN R., FRANKE W. EMBL/GENBANK/DDBJ DATA BANKS.
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EXTRACELLULAR
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                                                                                                                        ZIMBELMANN
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                                            MANABE M.
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TISSUE-KERATINOCYTES;

MEDLINE; 91271279_.

WHEELER G.N., PARKER A.E., '
ARNEMANN J., RUTMAN A.J., P.
BUXTON R.S., MAGEE A.I.;
                                                                                                                                                                              01-OCT-1993
01-OCT-1993
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X58466; G307; -. EMBL; X57784; G436062; -. EMBL; M58165; G552318; -. PIR; S14603; IJBOG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright.
                                                                                                                    EUKARYOTA;
                                                                                                                                                                 DESMOGLEIN 1
                                                                                                                                                                                                                                      DSG1_HUMAN
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                                                                            EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              97 YGIFVINQKTGEINI 111
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1 FGIFVVDKNTGDINI 15
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TISSUE SPECIFICITY: EPIDERMIS, MUZZLE, TONGUE AND
DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DESMOSOMAL SUBFAMILY
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                                                                                                                    SAPIENS (HUMAN).
RYOTA; METAZOA; CHORDATA; VERTEBRATA;
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                                                                                                                                                             3 (REL. 27, C)
3 (REL. 27, L)
7 (REL. 35, L)
1 PRECURSOR
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LAST SEQUENCE UPDATE)
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                                                                                                      HOMINIDAE;
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                                                                                                                                                                 (DESMOSOMAL
                  , THOMAS
                                                                                                                                                                                                                                                                                                                                                     Score 84; DB 1; I
Pred. No. 4.50e-06;
5; Mismatches 1
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CADHERIN 4.
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13898584 CRC32;
                S.C.,
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PREMOGLEIN 2 PRECURSOR (HDGC).
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Matches 9; Conse
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PROC. N
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-I. FUNCTION: COMPONENT OF INTERCELLUAR DESMOSOME JUNCTIONS.

-INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDI
FILAMENTS MEDIATING CELL-CELL ADHESION.

-I. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I. TISSUE SPECIFICITY: EPIDERMIS, TONGYLAND OESOPHAGUS.

-I. DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; YERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S16906;
MIM; 125670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute.
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                                        PRIMATES; CATARRHINI;
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SIMILARITY: BELONGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; PF00028; cadherin;
                                                                                                                                                                                                                                                                                                           FGIFVVDKNTGDINI
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                                        HOMINIDAE;
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Pred. No. 4.50e-06;
5; Mismatches 1
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CYTOPLASMIC
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Query Match
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Matches
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"Identification of the ubiquitous human
expression catalogue of the desmoglein s
cadherins.";
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HSSP; P15116; 1
CELL ADHESION;
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete amino acid sequence of the epidernal desn polypeptide and identification of a second type of EUR. J. CELL BIOL. 55:200.208(1991).

-i- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS
                                                                                                                                                                                                                                                                             REPEAT
REPEAT
REPEAT
                                                                              SEQUENCE
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MIM; 125671; -
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY
TISSUE SPECIFICITY: ALL OF THE TISSUES TESTED AND
DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE
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  Similarity 60.0% 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RES. 211:391-399(1994).
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DESMOGLEIN
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EXTRACELLULAR
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    Mismatches
                                                                              84D3B898 CRC32;
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epidermal desmoglein precursor
second type of desmoglein gene.";
                                       DB 1;
                                                                                                                                                                                                 N REPEAT
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                                       Length 1117;
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    Indels
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AND INTERMEDIATE
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    Gaps
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MEDLINE; 91239591.

MECHANIC S., RAYNOR K., I

"Desmocollins form a dis-
adhesion molecules.",

PROC. NATL. ACAD. SCI. U
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01-FEB-1994 (REL.
01-FEB-1994 (REL.
15-DEC-1998 (REL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              "Desmosomal glycoproteins 2 and 3 (desmocollins) show N-terminal similarity to calcium-dependent cell-cell adhesion molecules."; CELL SCI. 97:239-246(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 133-155.
MEDLINE; 91115997.
HOLTON J.L., KENNY T.P.,
SHARMA R., GARROD D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 133-893 FROM TISSUE-MUZZLE EPITHELIUM; MEDLINE; 92008912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 91185
COLLINS J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA;
ARTIODACTYLA; RUMINA
                                                                                                                                                                                                                                                                                                                                                                          PARRISH E.P., MARSTON GARROD D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pifferentiation 47:29-36(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GARROD D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE, FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRANKE W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. CELL BIOL. 113:381-391(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-EP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DESMOCOLLIN
                                                                                                                                                                                                                                                                                                                                                         Size heterogeneity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and sequence analysis (desmocollins): cadherin-like c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence
rom cloned cDNA: a n
                                                                                                                                                                                                                                                                                                             desmosomal glycoproteins 2
CELL SCI. 96:239-248(1990)
- FUNCTION: COMPONENT OF IN
                                                                                                                                                                                     FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO EPIDERMAL CELL POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS. LINKED TO THE KERATINIZATION OF EPITHELIAL TISSUES SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: EPIDERMIS AND WEAKLY IN TONGUE PAPILLAE.

DOMAIN: CRALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                                                                            PTM: FORM 1A IS PHOSPHORYLATED ON A SERINE BUT FORM 1B IS NO ALTERNATIVE PRODUCTS: TWO FORMS; 1A OR DG2 (SHOWN HERE) AND DG3; ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS TO THE
                                                                                                     DESMOSOMAL SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A. (1B), AND PARTIAL SEQUENCE
               non-profit
and this s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1A/1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEGAN P.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28,
37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37, LAST ANNOTATION UPDATE)
PRECURSOR (DESMOSOMAL GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (18),
          institutions as long atement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of bovine muzzle epithelial desmocollin derived covel subtype of desmosomal cadherins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   distinct
                                                                                                                                                                                                                                                                                                                                                          phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                     J.E.,
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LAST SEQUENCE UPDATE)

LAST ANNOTATION UPDAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEGAN P.K., COLLINS J.E., KEEN J.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KENNY T.P.,
                                                                                                                                                                                                                                                                                                                                           N
                                                                                                                                                                                                                                                                                                                                                                                     MATTEY D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WALSH M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                      ylation and transmembrane organisation and 3 (desmocollins) in MDCK cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subset of the cadherin family of cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           desmosomal adhesion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88:4476-4480(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of desmosomal glycoproteins 2 and desmosomal adhesion molecules with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COWIN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MACGARVIE
                                                                                                                                                                                                                                                                                                                                                                                     MEASURES H.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIMBELMANN R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUTHERIA; BOVINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOLTON
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RESULT
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Best Local
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01-NOV-1997
15-DEC-1998
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CONFLICT
SEQUENCE
                                          MEDLINE; 9328524...

MEDLINE; 9328524...

THEIS D.G., KOCH P.J., FRANNE ...

"Differential synthesis of type 1 and "Differential synthesis."; human stratified epithelia."; human stratified epithelia."; human stratified epithelia.";
                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
CARBOHYD
VARIANT
VARIANT
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REPEAT
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REPEAT
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EMBL;
SEQUENCE FROM N.A.
                           SEQUENCE FROM N.A.
TISSUE-FORESKIN;
                                                                                                                      EUKARYOTA;
                                                                                                                                             DESMOCOLLIN
                                                                                                                                                                                                                                                                                                                                                                     REPEAT
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                                                                                       EQUENCE FROM N.A.
ISSUE-FORESKIN;
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A43838;
A39377;
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X58029; G453584; -.
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X56968; G314
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X56966; G316; -.
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                                                                                                                                                                                                                                                    Similarity
                                                                                                              CATARRHINI;
              (JUN-1994)
                                                                                                                     NS (HUMAN).
METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        email
                                                                                                                                            (REL.
(REL.
(REL.
1A/1B
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                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               GLYCOPROTEIN;
                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             cadherin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CADHERIN;
dherin; 4.
                                                                                                                                            PRECURSOR
                                                                                                                                                                                                                             192
                                                                                                                                                                                                                                                                          893
485
99647
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                                                                                                                                                                                                                                                    62.9%;
53.8%;
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LAST SEQUENCE UPDATE)

LAST ANNOTATION UPDATE)

LAST ANNOTATION UPDATE)

(DG2/DG3)
                                                                                                              HOMINIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                        CALCIUM-BINDING;
              EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                           ₩,
                                                                                                                                                                                                                                            Score 66; DB 1; Len
Pred. No. 5.11e-02;
                                                                                                                                                                                                                                                                                1B/DG3).
MISSING (IN FORM 1B/DG3).
T -> A (IN REF. 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                     CADHERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION; TRAN
I-BINDING; ALTERNATIVE
                                                                                                                                                                                                                                                                                                        KVYLCGQDEEH ->
                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                     CADHERIN
                                                                                                                                                                                                                                                                                                                                                                           CADHERIN
                                                                                                                                                                                                                                                                                                                                                                                   CADHERIN
                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                         DESMOCOLLIN 1A/1B.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                         -> A (IN REF. 2 FF5DD78B CRC32;
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                                                                  type
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                                                                                                                      MAMMALIA; EUTHERIA
                                                                  N
                                                                                                                                                                                                                                                                                                       ESIRGHTLVKN
                                                                  desmocollin
                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEMBRANE;
                                                                                                                                                                                                                                                           Length 893;
                                                                                                                                                                                                                                             Indels
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                                                                  mRNAS
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                                    Query Match
Best Local
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EMBL;
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                                                                                    VARSPLIC CONFLICT
                                                                                                                      CARBOHYD
CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                MIM; 125643; -.
PROSITE; PS00232; CADHERIN; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE; 91323543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning of the cDNA (DSC1) coding its assignment to chromosome 18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-SKIN;
MEDLINE; 94116981
                                                                                                                                                                                                                                                                                                         CELL ADHESION;
                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENOMICS 18:185-194(1993).
                                                                                                                                                                                 REPEAT
REPEAT
                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                            CYTOSKELETON;
                                                                                                                                                                                                                                 TRANSMEM
                                                                       SEQUENCE
                                                                                                                                                           REPEAT
                                                                                                                                                                                                                       DOMAIN
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182 FNLFYIEKDTGDI 194
                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL
ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS. LINKED
TO THE KERATINIZATION OF EPITHELIAL TISSUES.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: STRONGLY EXPRESSED IN EPIDERMIS, LESS IN LYMPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
ALTERNATIVE PRODUCTS:
DG3; ARE PRODUCED BY A
SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVI
IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS
MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO EPIDERWAL CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: CALCIUM MAY BE BOUND BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DESMOSOMAL SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NODE AND TONGUE
                                                                                                                                                                                                                                                                                                                                                                  234522; G505538; -. 234522; G505537; -. X72925; G457463; -. X72925; G457464; -.
                                                                                                                                                                                                                                                                                                                    P09803;
                      h 61.9%; similarity 53.8%; 7; Conservative
                                                                                    841
132
                                                                                                                                                                                                                                                                                                                    1EDH.
                                                                                                                                                                                                                                                                                            CALCIUM-BINDING;
                                                                                                                                                                                                                                                                                           GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL; CALCIUM-BINDING; ALTERNATIVE SPLICING.
                                                                       AA;
                                                                                    894
132
                                                                                                                                              894
242
354
471
575
165
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                                                                       100044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : TWO FORMS; 1A OR DG2 (SHOWN HERE) AND ALTERNATIVE SPLICING OF THE SAME GENE. TO THE CADHERIN FAMILY. BELONGS TO THE
                                                                         ¥.
                                   Score
Pred.
                                                                                                                                                                                                                                                                                                                                            Ψ
                                                                                                                                                       CYTOPLASMIC
CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 4.
                                                                                 MISSING (IN FORM 1B/DG3).
T -> S (IN REF. 3).
                                                                                                                     KVYLCGQDEEH -> ESIRGHTLIKN
                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                        DESMOCOLLIN 1A/1B
                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                            1B/DG3
                                                                       A287BCA9 CRC32;
                         Mismatches
                                   No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the expression of DGII/III.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THE CADHERIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BUXTON R.S.;
                                     œ
                                    DB 1; I
8.27e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human type 1 desmocollin and
                                                                                                                                                                                                                      (POTENTIAL)
                                              Length 894;
                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a new
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FGIFVVDKNTGDI

Query Match Best Local

Similarity

58.1%; 46.2%;

Score Pred.

% 61;

DB 1; Length 886; 5.44e-01;

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01-NOV-1997
15-JUL-1998
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MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
EUKARYOTA; METAZOA; CHORDAE; MURIDAE; MURINAE; MUS.
  CARBOHYD
CARBOHYD
VARSPLIC
VARSPLIC
SEQUENCE
                                                                                                                           REPEAT
REPEAT
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REPEAT
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11. FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS, INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION, MAY CONTRIBUTE TO EPIDERMAL CELL POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS. LINKED TO THE KERATINIZATION OF EPITHELIAL TISSUES.

1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- ALTERNATIVE PRODUCTS: FORMS 1A AND 1B ARE PRODUCED I SPLICING OF THE SAME GENE.
-i- SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P55849;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                       CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X97986; E246528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. To
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35, LAST SEQUENCE UP
36, LAST ANNOTATION
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CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
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POTENTIAL.
POTENTIAL.

EVILCEGAEEH -> ESIRGHTLIKN

MISSING (IN FORM 1B).

6C3C94BA CRC32;
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                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₿
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                               TP2B_MOUSE STAT
Q6451;
15-JUL-1998 (REL. 3
15-JUL-1998 (REL. 3
15-DEC-1998 (REL. 3
DNA TOPOISOMERASE I
TOP2B.
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15-JUL-1998 (REL. 3
15-DEC-1998 (REL. 3
DNA TOPOISOMERASE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X86455; G790988; -
PROSITE; PS00177; TOPOISOMERASE_II;
PROSITE; PS00177; TOPOISOII; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entitles requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TP2B_CRILO
Q64399;
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1 FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY
BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS.

MAKES DOUBLE-STRAND BREAKS.

1 CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAC
OF DOUBLE-STRANDED DNA.

1 SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UEKEUDDRE S., FREY S., DELAPORTE C., JACQUEMIN-SABLON "Cloning and characterization of full-length cDNAs cod topoisomerase II beta from Chinese hamster lung cells resistant 9-OH-ellipticine.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00204; DNA_topoisoII; HSSP; P06786; 1BGW.
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   MUS MUSCULUS
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MEDLINE; 96085121
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NEGATIVE SUPERCOILS.
SIMILARITY: BELONGS TO TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS.
EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH
POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES
                                                                                                                                                                                                                                                                                                                                                                 2 IFVVDRNTVEI 932
|||||:||:|
3 IFVVDKNTGDI 13
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8; Conse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOISOMERASE; DNA-BINDING; ATP-BINDING; NUCLEAR PROTEIN.
814 814 DNA CLEAVAGE (BY SIMILARITY).
1612 AA; 182074 MW; AA9562E7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.1%;
larity 72.7%;
Conservative
(MOUSE)
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37,
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36, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDAT
II, BETA ISOZYME (EC 5.99
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                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
BETA ISOZYME (EC 5.99.1.3).
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Pred. No.
2; Misma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1612;
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RELAX ONLY
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TOPOISOMERASE II
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RESOLUTION AND SELECTION AND S
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Best Local
                                                                                                                                                                                                             MEDLINE; 93087165.

MEDLINE; 93087165.

JENKINS J.R., AYTON P., JONES T., DAVIES S.L., JONES T., DAVIES T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993
01-OCT-1993
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISOMERASE;
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA;
RODENTIA; S
                                                 SEQUENCE FROM N.A.
MEDLINE; 93192319.
AUSTIN C.A., SNG J.H., PATEL S., FISHER L.M.;
NOVEL HeLA topoisomerase II is the II beta isoform: com
sequence and homology with other type II topoisomerases.
BIOCHIM. BIOPHYS. ACTA 1172:283-291(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00177; TOPOISOMERASE_II; PFAM; PF00204; DNA_topoisoII; 1. HSSP; P06786; 1BGW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIYAIKE M., ADACHI N
SUBMITTED (SEP-1994)
   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 93087165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIMATES;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:98791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
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FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY
BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS.
MAKES DOUBLE-STRAND BREAKS.
CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAG
OF DUBLE-STRANDED DNA.
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SUBCELLULAR LOCATION: NUCLEAR; NUCLEAUS.
EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH
POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES
NEGATIVE SUPERCOILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAPIENS (HUMAN).
RYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATARRHINI;
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SCIUROGNATHI; MURIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOISOMERASE; DNA-BINDING; ATP-BINDING; NUCLEAR PROTEIN.
814 814 DNA CLEAVAGE (BY SIMILARITY).
1612 AA; 181863 MW; B496E4B5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REL.
(REL.
   1038-1271
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ACHI N., KIKUCHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOP2B
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27, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDAT
II, BETA ISOZYME (EC 5.99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.1%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMINIDAE;
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Pred. No.
2; Misma
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\E; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             re 61; DB 1; Le
1. No. 5.44e-01;
Mismatches 1;
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MUS.
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                                                                                                                                                                   RESULT
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Best Local S
Matches
                                                           15-JUL-1998
15-JUL-1998
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"Human cells express two differentially spliced
"Opolisomerase II beta mRNA.";
NUCLEIC ACIDS RES. 21:3719-3723(1993).
-!- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF D
BREAKAGE AND SUBSEQUENT REJOINING OF DNA STR
MAKES DOUBLE-STRAND BREAKS.
-!- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE,
OF DOUBLE-STRANDED DNA.
                                                                                                                        TP2B_CHICK
042131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Isolation and characterization of a human novel DNA topoisomerase II homologue from FEBS LETT. 266:115-117(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. entities requires a license agreement (See or send an email to license@lsb-sib.ch).
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                                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00204; DNA_topoisoII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use
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AUSTIN C.A.,
    GALLUS
                     TOP2B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATIVE SPLICING MEDLINE; 93376494.
                                                                                                                                                                                                                            934 IFVVDRNTVEI 944
|||||:|| :|
3 IFVVDKNTGDI 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISSP; P06786; 1BGW
ISOMERASE; TOPOISON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L; X68060; G37231; -.
L; X71911; -; NOT_ANNOTATED_CDS.
L; Z15111; G288567; -.
L; Z15115; G288565; -.
L; X3662; G38325; -.
; S26730; S26730.
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EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH
EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS: TWO FORMS, PRODUCED BY ALTERNATIVE SPLICING
                                         TOPOISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S26730;
S10710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POSITIVE SUPERCOILS, WHEREAS NEGATIVE SUPERCOILS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HOMODIMER.
  GALLUS
                                                                                                                                                                                                                                                                                                                  Similarity 72.7%, 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00177; TOPOISOMERASE_II;
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                                                                                                                                                                                                                                                                                                                                                                                                                        1611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOISOMERASE; DNA-BINDING; ATP-BINDING; PHOSPHORYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                       1626 AA;
                                                           (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPLICING; NUCLEAR PROTEIN 826 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FISHER L.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S41641.
(CHICKEN)
                                                                                                                                              STANDARD;
                                  36, CREATED)
36, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDATE)
II, BETA ISOZYME (EC 5.99.1
                                                                                                                                                                                                                                                                                                                                                                                                                           1611
                                                                                                                                                                                                                                                                                                                                       58.1%;
72.7%;
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2; 1
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                                                                                                                                                                                                                                                                                                                                                                                                  DNA CLEAVAGE (BY SIMILARITY).
MISSING (IN BETA-1).
T -> A (IN REF 2).
W; 4191FFFD CRC32;
                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                       NO .
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OF THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           There are no restrictions
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TOP2B G
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                                                                                                                                                                                                                                                                                                                                                           Length 1626;
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GENE. THE B
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RELAX ONLY
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TOPOISOMERASE II
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Matches
                                                           SEQUENCE FROM N.A.
STRAIRS / MG1655;
MEDLINE; 97426617.
BLATTNER F.R., PLUNKETT G
RILEY M., COLLADO-VIDES J
GREGOR J., DAVIS N.W., KI
MAU B., SHAO Y.;
                                                                                                                                                                                                  01-NOV-1995
01-NOV-1995
01-NOV-1997
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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NEOGNATHAE; GALLIFOI
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                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                 P46857;
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HSSP; P06786;
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BACTERIA; PROTEO
                                                                                                                                                                                          HYPOTHETICAL
                                                                                                                                                SCHERICHIA.
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FUNCTION: CONTROL OF TOPOLOGICAL STRAYES OF DNA BY TRANSIENT
BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE IJ
MAKES DOUBLE-STRAND BREAKS (BY SIMILARITY).
CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING
OF DOUBLE-STRANDED DNA.
SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTIC TOPOISOMERASE POSITIVE SUPERCOILS, WHER NEGATIVE SUPERCOILS.
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(REL.
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72.7%;
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, LAST SEQUENCE UPDATE)
, LAST ANNOTATION UPDATE)
PROTEIN IN GNTR-GGT INTE
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PHASIANIDAE; PHAS
                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-BINDING; ATP-BINDING;
DNA CLEAVAGE (BY SIMIL
POLY-GLY.
                                                                                                                                                          GAMMA SUBDIVISION;
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Swiss Institut Bioinformatics

"The complete genome sequence of SCIENCE 277:1453-1474(1997).

T G. III, BLOCH C.A., PERNA N.T., S J., GLASNER F.D., RODE C.K., MA-KIRKPATRICK H.A., GOEDEN M.A., R

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDH14.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VER
                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHIBATA T., SHIMOYAMA Y., GOTOH M., HIROHASHI S.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
SORTING OF HETEROGENOUS CELL TYPES.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998
15-JUL-1998
15-JUL-1998
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                                                                                                                        REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U59325; G1389853; -. PROSITE; PS00232; CADHERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL PROTEIN. SEQUENCE 94 AA; 10
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                                                                                                                                                                                                                                                                                                                                   ADHESION; GLYCOPROTEIN; PHOSPHORYLATION; TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                          PF01049; Cadherin_C_term; P15116; 1NCI.
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Pred. No. 8.60e-01;
6; Mismatches C
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CADHERIN 2.
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VARIANT
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P56121;
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PIR; JQ1917; JQ1917.
PFAM; PF00680; RNA_dep_RNA_pol; 1.
PFAM; PF00910; RNA_helicase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GENOME POLYPROTEIN (CONTAINS: 22.5 KD PROTEIN; 26 KD PROTEIN; 31 KD PROTEIN; PROBABLE RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48)).
PARSNIP YELLOW FLECK VIRUS (ISOLATE P-121) (PYFV).
VIRUSES; SERNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; SEQUIVIRIDAE;
SEQUENCE FROM N.A.
STRAIN-26695 / ATCC 700392.
                                                                 HELICOBACTER.
                                                                                 HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
BACTERIA; PROTEOBACTERIA; EPSILON SUBDIVISION;
                                                                                                                                  RNHB OR HP1323
                                                                                                                                                                                                                                                                                                                                                                                                   2246 FGVFGVNDTIGIIDV 2260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLYPROTEIN; ATP-BINDING; CO
RNA-DIRECTED RNA POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See Por send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 93107855.
TURNBULL-ROSS A.D., REAVY
"The nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q05057
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                                                                                                                                                          RIBONUCLEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      picorna-like virus.";
J. GEN. VIROL. 73:3203-3211(1992).
-!- SIMILARITY: SOME, TO THE CMPV AND TBRV POLYPROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 93107855.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                6
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                                                                                                                                                (REL. 35, | (REL. 35, | REL. 35, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.1%;
larity 58.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REAVY B., MAYO M.A., MURANT A.F.; sence of parsnip yellow fleck virus:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88072 MW;
                                                                                                                                                , CREATED)
, LAST SEQUENCE UPDATE)
, LAST ANNOTATION UPDATE)
3.1.26.4) (RNASE HII)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COAT PROTEIN; TRANSFERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 58; D
Pred. No. 2.
4; Mismato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WW; ->
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Pred. No. 8.60e-(
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T -> I.
                                                                                                                                                                                                                                                                   PRT;
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2.12e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JB 1,
60e-01;
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 790;
                                                                                      HELICOBACTER GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Search completed: Fri Jun 11 17:16:12 1999 Job time: 8 secs.
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                                                                                                                                                                                                                                                                                                           Query Match 54.3%;
Best Local Similarity 46.2%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                EMBL: AE000634; G2314491; -.
TIGR: HP1323; -.
HYDROLASE; NUCLEASE; ENDONUCLEASE; MAGNESIUM.
SEQUENCE 209 AA; 23176 MW; FA2B072C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAJORI.";
NATURE 388:539-547(1997).
-I- EUNCTION: DEGRADES THE RIBONUCLEOTIDE MOIETY ON RNA-DNA HYBRID MOLECULES (BY SIMILARITY).
-I- CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE TO 5'-PHOSPHO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 97394467.

TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,
FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.,
FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.,
NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S.,
LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A.,
MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K.,
BERG D.E., GOCAYME J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M.,
COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATTHEY L., WALLIN E.,
HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MONOESTER.
-!- SIMILARITY: WITH OTHER RNASE H FROM BACTERIA, FUNGI, AND WITH RNASE H DOMAINS FROM POL OF RETROVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VENTER J.C
                                                                                               67 GFFVVKKSANEID 79
|:||| |::::|:
2 GIFVVDKNTGDIN 14
                                                                                                                                                                                           Score 57; DB 1; Length 209; Pred. No. 3.30e+00; 5; Mismatches 2; Indels
                                                                                                                                                                                                 0
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:16:29 1999; MasPar time 6.21 Seconds 131.825 Million cell updates/sec

Tabular output not generated...

Description:
Perfect Score:
Sequence: Title: >US-08-991-628-2 (1-15) from US08991628.pep 105

1 FGIFVVDKNTGDINI 15

Scoring table: PAM 150 Gap 15

Searched: 179066 segs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb19

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 26.631; Variance 35.345; scale 0.753

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Ç.	19	18	17	16	, <u>, , , , , , , , , , , , , , , , , , </u>	14	13	12	11	10	·	· œ	7	σ	, UI	4	·w	N		No.
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54.3	54.3	55.2	ū		ú	Ü	55.2	U	U	σ	σ	σ	σ	7	57.1	58.1	60.0	62.9	85.7	Query Match
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Q15066	057984	060247	060246	060245	057537	093508	075284	065522	028514	033373	048662	Q58723	Q58735	029907	Q55701	Q24292	076356	Q90763	035902	Ħ
OB-CADHERIN-2.	504AA LONG HYPOTHETICA	PCDH7 (BH-PCDH)C.	PCDH7 (BH-PCDH)B.	PCDH7 (BH-PCDH)A.	NF-PROTOCADHERIN.	PARAXIAL PROTOCADHERIN	KIAA0345-LIKE 9.	HYPOTHETICAL 68.6 KD P	CONSERVED HYPOTHETICAL	PILC PROTEIN.	PV72.	HYPOTHETICAL PROTEIN M	HYPOTHETICAL PROTEIN M	ALDEHYDE FERREDOXIN OX	HYPOTHETICAL 24.5 KD P	ADHERIN.	C45G7.6 PROTEIN.	CHICKEN CADHERIN-7.	DESMOGLEIN 3 (FRAGMENT	Description
6.41e+00	6.41e+00	4.15e+00	4.15e+00	4.15e+00	4.15e+00	4.15e+00	4.15e+00	4.15e+00	4.15e+00	2.68e+00		2.68e+00	2.68e+00	1.72e+00	1.72e+00	1.10e+00	4.40e-01	1.08e-01	4.88e-07	Pred. No.

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1616	σ	σ	σ	4	æ	790	569	437	340	261	211	143	112	831	601	423	205	171	814	803	798	797	794	792
14	4	φ	N	N	4	3	14	10	10	13	ш	N	<u>بــ</u>	S	N	10	ري.	տ	4	4	N	11	13	13
P89676	ω 5	\mathbf{r}	Q53550	Q45916	Q15855	Q90762	Q69013	022141	022706	042389	029130	066117	Q58642	P91388	യ	065875	Q27742	061171	075281	075283	Q50288	Q63418	093264	093319
	READTHROUGH STOP CODON	ANTP-139.	PROGENITOR TOXIN L NON	138KDA PROTEIN ASSOCIA	UVOMORULIN PRECURSOR (CHICKEN CADHERIN-6B.	POLYMERASE (FRAGMENT).	PUTATIVE NUCLEOTIDE SU		ALTASE (F	HYPOTHETICAL 23.4 KD P	16.3 KD	HYPOTHETICAL PROTEIN M	COSMID K12D9.	PUTATIVE TRANSPORT SYS	CELL DIVISION PROTEIN	GLUTATHIONE PEROXIDASE	CENTRIN 1 (FRAGMENT).	KIAA0345-LIKE 6.	KIAA0345-LIKE 8.	PUTATIVE LIPOPROTEIN.	PROTOCADHERIN 3.	CADHERIN PRECURSOR.	CADHERIN 11.
	1.50e+01	1.50e+	1.50e+	1.50e+01	1.50e+01	1.50e+01					1.50e+01			9.83e+00		9.83e+00		9.83e+00	٠		6.41e+00	6.41e+00	6.41e+00	6.41e+00

ALIGNMENTS

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GALLUS GALLUS (CHICKEN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES; NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS. [1]	-1996 (7 -1996 (7 -1999 (7	LT 2 Q90763 PRELIMINARY; PRT; 785 AA. Q90763.	97 FGIFVVDPNNGDINI 111 1 FGIFVVDKNTGDINI 15	Query Match 85.7%; Score 90; DB 11; Length 993; Best Local Similarity 86.7%; Pred. No. 4.88e-07; Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	TER 993 993 ENCE 993 AA; 107888 MW; 881794BD CRC32;	PROSITE; PS00232; CADHERIN; 2. PFAM; PF00028; Cadherin; 4. CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; CALCIUM-BINDING; REPEAT.	PROTE	ISHIKAWA H., LI K., UITTO J.; SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.	SEQUENCE FROM N.A. STRAIN-BALB/C;		MUS MUSCULUS (MOUSE). EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALTA: EHTHERTA: RODENTTA:	DESMOGLEIN 3 (FRAGMENT).	8 (TREMBUREL.	(TREMBLREL. 05, CREATED)	LT 1 035902 PRELIMINARY; PRT; 993 AA. 035902:

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RESULTING COLUMN AND C
  Query Match
Best Local S
Matches
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Best Local S
Matches
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01-NOV-1998 (TRE
01-NOV-1998 (TRE
01-NOV-1998 (TRE
C45G7.6 PROTEIN.
C45G7.6.
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM SEQUENCE FROM STRAIN-BRISTOL N2;
DANTE M., WAMSLEY P.;
"The sequence of C. elegans cosmid C45G7.";
The sequence of C. elegans cosmid C45G7.";
The sequence of C. elegans cosmid C45G7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CORAKTON M., DEAR S., DU Z., DURBIN, R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLACHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPEA SAUNDERS D., SHOWKEEN
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
TO MATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           076356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                           SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ
-:- SUBCELLULAR LOCAFION: TYPE I MEMBRANE
EMBL; AF067611; G13193145; -.
PROSITE; PS00233; CADHERIN; 1.
CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE
CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 95309115.
NAKAGAWA S., TAKEICHI M.;
"Neural crest cell-cell a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SIKAIN-WHITE LEGHORN; TISSUE-BRAIN;
  Local Similarity
nes 8; Conser
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  Conservative
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9 AA; 146518 P
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STRAIN-PCC6803;
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KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKA KANEKO T., SATO S., KIMURA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAWOTO S., KIMURA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., Y
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01-NOV-1996
                                                                                                                                                                                                                                                                                    KANEKO T., TANAKA A., SATO S., KOTANI H., SAZUKA T., MIYAJIMA N., SUGIURA M., TABARA S.;
"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. sequence features in the 1Mb region from map positions 64% to 92% of the genome.";
DNA RES. 2:153-166(1995).
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EUKARYOTA;
PTERYGOTA;
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CELL ADHESION; GLYCOPROTEIN;
SEQUENCE 3380 AA; 366356 )
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GENES DEV. 9:1530-1542(1995)
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PS00232; CADHERIN;
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METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSE
DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
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                                          NAKAMURA Y.,
IMURA T.,
JO K., OKUMURA S.,
M., YASUDA M.,
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KLENK H.-P., CLAYTON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
KERLANDAGE A.R., GRAHAM D.E., KYRPIDES N.C.,
RICHARDSON D.L., KERLANVAGE A.R., GRAHAM D.E., KYRPIDES N.C.,
FLEISCHAMAN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.
KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B
PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZH
OVERBEEK R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK
COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M.,
SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
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METHANOCOCCUS JANNASCHII
ARCHAEA; EURYARCHAEOTA; 1
METHANOCOCCUS.
                                                                                                  01-JUN-1998 (TREMBLREL. 06, 01-JUN-1998 (TREMBLREL. 06, 01-JUN-1998 (TREMBLREL D6, 101-JUN-1998 (TREMBLREL D6, HYPOTHETICAL PROTEIN MJ1339 MJ1339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sulphate-reducing archaeon NATURE 390:364-370(1997).
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01-JAN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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EMBL; D64000; D1010882; -.
HYPOTHETICAL PROTEIN.
SEQUENCE 214 AA; 24539 MW; CDEA936D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE001081; G2650295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-VC-16 / DSM
MEDLINE; 98049343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VENTER J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARCHAEOGLOBUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARCHAEOGLOBUS FULGIDUS.
ARCHAEA; EURYARCHAEOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF0340
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"Sequence analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The complete genome sequence of the hyperthermophilic, ulphate reducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQUENCE FROM N.A.
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Local Similarity 40.0%;
les 6; Conservative
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Similarity 42.9%;
6; Conservative
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REL. 05, LAST SEQUENCE UPDATE)
REL. 08, LAST ANNOTATION UPDATE)
OXIDOREDUCTASE (AOR-3).
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                             METHANOCOCCALES; METHANOCOCCACEAE,
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Pred. No. 1.
6; Mismatc
                                                                                                                                                                        CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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Pred. No. 1.72e+00;
7; Mismatches 1
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1.72e+00;
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LOFTUS B.,
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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RA SUTTON G.G., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,

RA SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,

RA KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,

RA COTTE J.L., GEOGHAGEN N.S.M., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,

RA SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,

RA UTTERBACK T.R., KEILEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,

RA COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M.,

RA KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
SCHOOLS
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Best Local S
Matches
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Best Local
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048662;
01-JUN-1998
01-JUN-1998
01-NOV-1998
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01-JUN-1998
01-JUN-1998
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BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D., SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D., SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D., KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I., OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., WERRICK J.M., GLODEK A., COTTOLL, GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D., SCOTT J.L., GEOGHAGEN N.S.M., PETERSON J.D., SADOW P.W., HANNA M.C., COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORDDOVSKY M., KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschil.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 8
Q58723
Q58723;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCIENCE 273:1058-1073(1996).

EMBL; U67573; G1591968; -.

HYPOTHETICAL PROPERIN.

SEQUENCE 245 AA; 28779 MW
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EMBL; U67574; G1591981; -.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                      151 YGIFVVDK 158
:||||||
1 FGIFVVDK 8
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Similarity 42.9%;
6; Conservative
                                          (TREMBLREL.) (TREMBLREL.)
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                                                                                                                                                   PRELIMINARY;
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87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              28779 MW;
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                                             866
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                                                                                                                                                                                                                                                                                                                                                      Score 59;
Pred. No.
1; Misma
                                          CREATED)
LAST SEQUENCE UF
LAST ANNOTATION
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 2.68e+00;
4; Mismatches 4
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CUCURBITA

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Best Local
Matches
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Best Loc
Matches
SEQUENCE FROM N.A.

STRAIN-VC-16 / DSM 4304 / ATCC 49558;

STRAIN-VC-16 / DSM 4304 / ATCC 49558;

MEDLINE; 98049343.

KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,

KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,

RICHARDSON D.L., KERLAYAGE A.R., GRAHAM D.E., KYRPIDES N.C.,

RICHARDSON D.L., CQUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,

FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,

FLEISCHMANN R.D., CONTIGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.
                                                                                                                                                                              028514
028514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       O33373;
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01-JAN-1998 (
01-AUG-1998 (
PILC PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEISSERIA
BACTERIA;
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                                                                                                             ARCHAEOGLOBUS FULGIDUS. ARCHAEA; EURYARCHAEOTA;
                                                                                                                                         01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
01-AUG-1998 (TREMBLREL.
CONSERVED HYPOTHETICAL E
                                                                                                                                                                                                                                                                                                               BARCKMAN M., KAELLSTROEM H., JONSSON A.B.;
MICROBIOLOGY 144:149-156(1998).
ENRIL; A4001121; E334755; -.
SEQUENCE 1033 AA; 112936 MW; B0593053
                                                                                                                                                                                                                                                                                                                                                       STRAIN-GC-653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; VIRIDIPLANTAE; STREI EUPHYLLOPHYTES; SPERMATOPHYTA;
                                                                                                      ARCHAEOGLOBUS.
                                                                                                                                   CONSERVED AF1760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUCURBITALES;
                                                                                                                                                                                                                                                      804 YGIFDDDKGTGTVKV 818
                                                                                                                                                                                                                                                                                                                                                               QUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                   Match
Local
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                                                                                                                                                                                                                                                                         Similarity 46.7%, 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 70.0% 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 GONORRHOEAE.
PROTEOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                        8 (TREMBLREL.
8 (TREMBLREL.
8 (TREMBLREL.
                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUCURBITACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COTYLEDON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.2%;
70.0%;
                                                                                                                                                                                                                                                                                  56.2%;
                                                                                                                                         . 05, CREATED)
. 05, LAST SEQUENCE UPDATE)
. 07, LAST ANNOTATION UPDAT
PROTEIN.
                                                                                                              ARCHAEOGLOBALES;
                                                                                                                                                                                                                                                                                                                                                                                                                           05,
07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; HYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSI
                                                                                                                                                                                                                                                                                                                                                                                   BETA
                                                                                                                                                                                                                                                                       Score
Pred.
4; M
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred.
2; M
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                                                                                                                                                                                                                                                                                                                                                                                    SUBDIVISION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                B0593053 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59;
                                                                                                                                                                                                                                                                                   No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1033
                                                                                                                                                                                           270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.68e+00;
                                                                                                                                                                                                                                                                                 DB 2; L
2.68e+00;
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                                                                                                              ARCHAEOGLOBACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                   NEISSERIACEAE;
                                                                                                                                                                                                                                                                          4;
                                                                                                                                                                                                                                                                                          Length 1033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                    NEISSERIA
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Best I
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Matches
                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                           Matches
SEQUENCE FROM N.A.
KIMMERLY W., BONDOC M., '
KADNER K., MIGUEL T., MI
SUBRAMANIAN S., MARTIN C
"Sequencing of human chr-
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
BEVAN M., BENES V., R.
MEWES H.W., MAYER K.F.
SUBMITTED (APR-1998)
                                                                                                                      075284;
01-NOV-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1998
01-AUG-1998
01-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LT 12
065522;
065522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A OVERBEEK R., GOCAYNE J.D., WELDMAN J.F., MCDONALD I.V. UTTER. COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYES S.M. SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A. MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R. VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence sulphate-reducing archaeon Arc NATURE 390:364-370(1997).
EMBL; AE000981; G2648791; -.
TIGR; AF1760; -
                                                              HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                              01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
KIAA0345-LIKE 9.
                                                                                                                                                                                                                                                                                   EU ARABIDOPSIS SEQUENCING PROJECT;
SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ
EMBL; ALOZES37; E1287270; -
HYPOTHETICAL PROTEIN.
SEQUENCE 593 AA; 68632 MW; 9EA10B88 CR
                                                                                                                                                                                                                                                                                                                               SEQUENCE
EU ARABID
                                                                                                                                                      075284
                                                                                                                                                                                                                                                                                                                                                                                                                   ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARXOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYTLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSI
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL
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SEQUENCE 270 AA; 29554
                                                                                                                                                                                                                      528
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Similarity 40.0%;
6; Conservative
                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                          FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TREMBLREL. 07, CREATED)
(TREMBLREL. 07, LAST SEQUENCE UPDATE)
(TREMBLREL. 07, LAST ANNOTATION UPDATE)
L 68.6 KD PROTEIN.
                                                                                                                                                                                                                                        55.2%;
larity 35.7%;
Conservative
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                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                              RECHMANN S., BORKOVA I
.F.X., SCHUELLER C.;
) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                     541
             M., CHENG J.,
, MILLER C., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
                                                                                                           888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nce of the hyperthermophilic, Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                          Score
Pred. :
7; M
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Pred.
5; }
                                                                                                          CREATED)
LAST SEQUENCE UI
LAST ANNOTATION
                                                                             VERTEBRATA;
                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                     9EA10B88 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E5FA8A9B CRC32
                     PITLUCK S., POLLARD M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                     58;
No.
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                                                                                                                                                                                                                                      DB 10; 4.15e+00; 2;
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4.15e+00;
                                                                                                                                                       816
                                                                                                                                                                                                                                                                                                                                                                                   , D.,
                                                                                                          ON UPDATE)
                                                                                                                                                                                                                                                                                                                      DATA
                                                                             MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                DATA
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                                                                             EUTHERIA;
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                      ROJESKI
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                                                                             PRIMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                               ROSIDAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 55.2%;
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local'Similarity 41.78;
      Query Match 55.2%;
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

YAMAMOTO A., DE ROBERTIS E.M.;

SUBMITTED (JAN'1998) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

EMBL; AF042191; G3201.662; -.

PROSITE; PS00232; CADHERIN; 5.

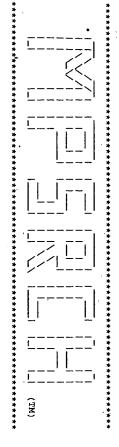
PROSITE; PS00232; CADHERIN; TRANSMEMBRANE; CALCIUM-BINDING; REPEA'

CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; CALCIUM-BINDING; REPEA'

SEQUENCE 950 AA; 105381 MW; 96B102F0 CRC32;
                                                                                                                    BRADLEY R.S., ESPESETH A., KINTNER C.;
CURR. BIOL. 0:0-0(1998).
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
EMBL; AF043643; G2852363; -.
PROSITE; PS00232; CADHERIN; 6.
CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; CALCIUM-BINDING; REPEA'
SEQUENCE 1035 AA; 113713 MM; 7E4D3C4E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 057537;
057537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System.";
SUBMITTED (SEP-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AC005609; G3540165; -.
                                                                                                                                                                                                                                                                                                                                                                                        XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEDOSTEI; EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; CYPRINOIDEA;
CYPRINIDAE; RASBORINAE; DANIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TREMBLREL 08, CREATED)
01-NOV-1998 (TREMBLREL 08, LAST SEQ
01-NOV-1998 (TREMBLREL 08, LAST ANN
PARAXIAL PROTOCADHERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBMITTED (SEP-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                093508;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NF-PROTOCADHERIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      615 LFSIDKNTGEI 625
:| :||||:|
3 LFVVDKNTGDI 13
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| |::: |||:|::
4 FVVDKNTGDINI 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A.
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Score 58; DB 13; Length 1035; Pred. No. 4.15e+00; 3; M1smatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 58; DB 4; I
Pred. No. 4.15e+00;
6; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 58; DB 13; Le Pred. No. 4.15e+00; 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3F41D941 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 950
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   0
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                                                                                                                                                    REPEAT
   Gaps
   0
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Db 552 GIFSIHPDTGDITV 565
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Qy 2 GIFVVDKNTGDINI 15
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Search completed: Fri Jun 11 17:18:36 1999 Job time : 127 secs.



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:27:18 1999; MasPar time 4.80 Seconds 66.422 Million cell updates/sec

Tabular output not generated.

Title: >US-08-991-628-3
Description: (1-15) from US08991628.pep
Perfect Score: 96

Sequence: 1 LNSKIAFKIVSQEPA 15

Scoring table: PAM 150
Gap 15

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38

statistics: Mean 18.085; Variance 51.973; scale 0.348

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
<u>,</u>	96	100.0	15	35	W78814	Desmoglein 3 protein	3.65e-04
N	96	100.0	15	20	W04843	Self epitope of desmo	3.65e-04
ω	96		15	ω	W64815	190	3.65e-04
4	96	100.0	614	19	W07908	Pemphigus vulgaris an	3.65e-04
u	96		. 999	σ	R30742	Human pemphigus vulga	3.65e-04
o	87	90.6	778	21	W15489	Pemphigus foliaceus a	5.06e-03
7	77	80.2	263	24	W13010	Segment of desmosomal	8.83e-02
œ	77	80.2	560	24	W13009	Segment of desmosomal	8.83e-02
9	54	56.3	878	10	R55060	Sequence of human liv	4.45e+01
10	54	56.3	878	15	R85487	Human E-cadherin prec	4.45e+01
11	54	56.3	2233	ω W	W48711	HPIV-3 JS isolate wil	4.45e+01
12	54	56.3	2233	ω	W48712	HPIV-3 FRhl cp45 vacc	4.45e+01
13	54	56.3	2233	33	W48713	HPIV-3 Vero cp45 vacc	4.45e+01
14	53	55.2	456	37	W82841	Human cerebral protei	5.74e+01
15	49	51.0	572	œ	R40843	Bilirubin oxidase.	1.57e+02
16	49	51.0	916	21	W13129	Full length human cad	1.57e+02

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R13516 R35199 W20828	R98226 R99579	R97628 W34554 W49858 W38455	W79334 R97629 R97630 R97631	R30730 R30177 R97246	W75000 W89745 W74883 R75741 R75731	W24307 W60192 W20908 W23994 W23994 W23994 R67913 R06643
P.denitrificans COB N Mouse multidrug resis H. pylori cytoplasmic	uronal protein n large subuni	- M	StaphyLococcus aureus Human SLAM2 T-cell co Human SLAM3 T-cell co Human SLAM4 T-cell co	urgdorferi lence gene	Staphylococcus aureus Human secreted protei B31 outer surface pro B. burgdorferi strain	ation of ation of iophage solution inner the sodium c sodium an growth
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ALIGNMENTS

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Sequence

15

AA;

into phagocytic cells. treating genetic disea an immune response.

diseases,

infections or

can be used for gene therapy, e.g. for infections or tumours or for downregulating

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The intrinsic disease
That also is a sequence motified and and is a sequence motified as a sequence of class in individual to an acid correction.

CC (MBP) polypeptide which is capable of tolerising an individual to an automatigen; or an isolated human pathogen polypeptide correction of tolerising an individual to that polypeptide. In both cases, the polypeptide (whether self or non-self) includes an amino acid correction, such as HLA-DR, which is associated with a human autorisative disease and which binds to the polypeptide to activate autoreactive corresponding which binds to the polypeptide to activate autoreactive disease and which binds to the polypeptide to activate autoreactive corrections in individuals with the autoimmune disease. This peptide is derived from the human desmoglein 3 protein (amino acids 190-204) cand is implicated as a self epitope in pemphigus vulgaris. Peptides for a serived from the human desmoglein protein are described in W04841-47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W04843;
W04843;
                                                    29:SEP-1998 (first entry)
Desmoglein-3 190-204.
Desmoglein; DG; gene therapy; pemphigus vulgaris;
autoantigen; autoimmune disease; MHC.
                                                                                                                                W64815
W64815
                             Homo sapiens.
US5783567-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens - useful in disease treatment, and method for identification of other self and non-self antigens implicated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strominger JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAR-1995; US-400796.
(HARD ) HARVARD COLLEGE
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WO9627387-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-1997 (first entry)
Self epitope of desmoglein 3, implicated in autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nfluenza; haemagglutinin; reovirus; sigma protein
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1. No. 3.65e-04;
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3.65e-04;
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                                                                            microparticle;
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Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                    Fused protein recognised by pemphigus vulgaris auto:antibody - useful to treat and diagnose pemphis vulgaris claim 1; Page 7-9; 9pp; Japanese 1, 19pp; Vapanese 1, 19pp; Vapan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microparticle encapsulated nucleic acids expression of proteins e.g. in gene therapy Disclosure; Column 4; 42pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pemphigus vulgaris antigen protein extracellular region Autoantibody; immunoglobulin G; IgGl; fusion protein; ditreatment; pemphigus vulgaris; PV; bulla; blister; skin
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                                                    189
                                                                                                                                                                                                        pemphigus vulgaris.
Sequence 614 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-1995; 165632.
30-JUN-1994; JP-173291.
(NISH/) NISHUKAWA T.
WPI; 96-388562/39.
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1. No. 3.65e-04;
Mismatches 0;
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No. 3.65e-04;
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                                                                      foliaceus patient autoantibody which comprises the constant region of IgG linked to the extracellular region of pemphigus foliaceus antigen protein through the hinge portion. Pemphigus foliaceus is a chronic, generalised, vesicular and scaling skin eruption similiar to dermatitis herpetiformis. The pemphigus foliaceus antigen fusion protein is useful to treat pemphigus foliaceus. The antigen is especially administered through an acornent upon which the fusion protein is immobilised via a carrier. The fusion protein is also useful for detecting pemphigus foliaceus antibodies which is useful in immondiagnosis. The fusion protein has little or no side effect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and its encoding DNA may be used in the diagnosis and treatment pemphigus vulgaris. It is thought that the antigen may be a cell adhesion molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding pemphigus vulgaris antigen diagnostic and therapeutic uses Disclosure; Fig 7; 50pp; English. This sequence is the pemphigus vulgaris and its encoding DNA may be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-NOV-1991; 798918.
27-NOV-1991; US-7989918.
(USSH) US DEPT HEALTH & HUMAN SERVICE.
Amagai M, Klaus-Kovtun V, Stanley JR;
WPI; 93-067436/08.
                                                                                                                                                                                                                    Pemphigus foliaceus antigen-IgO constant region fusion protein through the hinge region used to treat pemphigus foliaceus Claim 1; Page 10-12; 17pp; Japanese.
This sequence represents a fused protein recognised by pemphigus
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pemphigus follaceus antigen-IgG constant region fusi
Pemphigus follaceus; autoantibody; constant region;
extracellular region; antigen; hinge portion; skin;
dermatitis herpetiformis; fusion protein; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; Q35992
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                                                                                                                                                                                                                                                                                                 (NISH/) NISHIKAWA T. WPI; 97-241758/22.
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12-SEP-1995; 260899.
12-SEP-1995; JP-260899.
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Pemphigus vulgaris; skin disease; autoantibodies;
keratinocyte cell surface antigen; glycoprotein;
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yuence 778 AA;
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Score 87; D
Pred. No. 5.
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Pred. No. 3.65e-04;
0; Mismatches (
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   Mismatches
                                DB 21;
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RESULT 7

ID W13010;

AC W13010;

DT 21-NOV-1

DE Segment

KW micromest

KW micromest

KW metastat

OS Homo saj

PN DE19531(

PN 23-AUG---

PR 23-AUG---

PR 23-AUG---

PR 23-AUG---

PR 23-AUG---

PR 1397

PA Antibod;

PT werface

PT useful:

PS Claim 9

CC dismogl.

CC desmogl.

CC directe

CC directe

CC directe

CC directe

CC detect

CC arcino

CC metasta

CC arcessi

CC carcino

SQ Sequenc
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7-FEB-1997.

7 27-FEB-1995; 031033.

R 23-AUG-1995; DE-031033.

R 23-AUG-1995; DE-031033.

R 23-AUG-1995; DE-031033.

R (PROG-) PROCEN BIOTECHNIK GMBH.

Pranke WW, Schaefer S;

R WPI; 97-146518/14.

R MPI; 97-146518/14.

Pranke of epithelial or carcinoma cells, not bound to desmosomes, useful for diagnosis and treatment of carcinoma micrometastases Claim 7; Page 5; 8pp; German.

The present sequence is a segment of the desmosomal cadherin (DC), desmoglein Dsg2, which is exposed on the surface of epithelial or carcinoma cells and not bound to desmosomes. An antibody (Ab) directed against epitopes of the present sequence can be used to
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27-FEB-1997.
23-AUG-1995; 031033.
23-AUG-1995; DE-031033.
(PROG-) PROGEN BIOTECHNIK GI
Franke WW, Schaefer S;
WPI; 97-146518/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a segment of the desmosomal cadherin (D desmoglein Dsg2, which is exposed on the surface of epithelial carcinoma cells and not bound to desmosomes. An antibody (Ab) directed against epitopes of the present sequence can be used to diagnose, i.e. to detect carcinoma cells, especially micrometastases, not bound to desmosomes, to separate, enrich o detect living or fixed carcinoma cells by cell sorting methods as a therapeutic to deliver agents, e.g. other Ab or toxins, to target cells. The Ab provides rapid and reliable detection of metastatic carcinoma, and detects parts of DC that are not accessible in desmosome bound cells, as in normal tissue or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody reactive with part of desmosomal cadherin - ex surface of epithelial or carcinoma cells, not bound to useful for diagnosis and treatment of carcinoma microme Claim 9; Page 5; 8pp; German
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Desmosomal cadherin; desmoglein; Dsg2; cell; surface; epithe carcinoma; desmosome; antibody; epitope; diagnosis; detectio micrometastasis; separation; enrichment; targetted delivery;
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W13009 standard; protein;
                                                                                                                                                                                                                                                                               Homo sapiens.
DE19531033-A1.
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cadherin; desmoglein; Dsg2; cell; surface; epithe
cadherin; atthody; epitope; diagnosis; detectio
desmosome; antibody; epitope; diagnosis; detectio
tasis; separation; enrichment; targetted delivery;
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8.83e-02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pri Purified human E-cadherin protein and nucleic acid - used to produce of develop prods. for diagnosis, prognosis, therapy and prophylaxis for develop prods. for diagnosis, prognosis, therapy and prophylaxis for develop prods. for diagnosis, prognosis, therapy and prophylaxis for fit-cadherin disorders, e.g. malignancies

Pri of t-cadherin disorders, e.g. malignancies

CC Laim 1; page 59-63; 97pp; English.

CC E-cadherin is a cell adhesion molecule that is also known as cure to the cell can repeat the laid to the DNA encoding hEC was obtd.

CC Libraries and a colonic epithelial cell CDNA library. The following consequences are specifically claimed; AAS 1-878; 151-878; 30

CC Libraries and a colonic epithelial cell CDNA library. The following convertial AAS from AAS 308-878; AAS 178-703; AAS 178-299; AAS 290-CC 401; AAS 402-513; AAS 178-513; AAS 151-703; AAS 178-299; AAS 290-CC 404; AAS 402-513; AAS 178-513; AAS 151-703; AAS 178-299; AAS 28-878; CC 404; AAS 402-513; AAS 178-513; AAS 151-703; AAS 178-290; ABS 728-878; CC 404; AAS 402-513; AAS 178-5286; 1332-3000; 540-1500; 348-906; 890-CC 2749; 566-2749; 1-1053; 510-2596; 1332-3000; 540-1500; 348-906; 890-CC 2749; 566-2749; DNA encoding at least 30 AAS selected from CC AAS 308-878. The prods. can be used in the diagnosis, prognosis, CC expression. Suitable dosages for i.v. admin. of a protein are CC 20-500 mcg/kg body wt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                          Human E-cadherin precursor.
E-cadherin; T-lymphocyte; alpha-E,beta-7 integrin;
auto1mmune disease; Crohn disease; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-1994.
16-NOV-1993; U11097.
17-NOV-1992; US-978897.
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WO9411401-A.
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                                                                                                                                                                    T 10
R85487 standard;
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Morrow JS, Rimm DL;
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  Homo
                                                                                                                 18-MAR-1996
                                                                                                                                               R85487
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                                                                                                                                                                                                                                                                                                                    293 naaiaytilsqdp 305
|: ||: |:||:|
                                                                                                                                                                                                                                                                                                                                                                                         56.3%;
Local Similarity 53.8%;
les 7; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
human liver E-cadherin.
Helial-cadherin; E-cadherin; cell adhesion molecule;
Helial-cadherin; Cell CAM 120/80.
                                                                                                                 (first entry)
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                                                                                                                                                                          Protein;
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73.3%;
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4; M
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No. 8.83e-02;
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19-SEP-1997; U16718.
27-SEP-1996; US-026823.
(AMCY ) AMERICAN CYANAMID CO.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
MURDY BR, RANDOLPH VB, Sidhu MS, Tatem JM
WPI; 98-230710/20.
N-PSDB; V18272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page. 70-75; 103pp; English.

The human E-cadherin protein precursor (R85487) is expressed by an cDNA clone (T05764) derived from human liver. The extracellular ancount of E-cadherin is used to generate peptides that specifically bind to heterotypic cognates of E-cadherin and which inhibit adhesion of intra-epithelial T-lymphocytes to E-cadherin-expressing epithelial or endothelial cells in vitro or in vivo, thereby modulating mucosal immune responses. Such peptides are also specifically reactive with a monoclonal antibody (E4.6 or E6.1) that binds to E-cadherin and that can inhibit T-cell binding.
                                        Recombinantly-generated, attenuated, non-segmented, negative-sense, single stranded RNA virus of order Mononegavirales - having attenuating mutation in 3' genomic promoter region and RNA polymerase gene, useful as vaccine to immunise against such virus pisclosure; Page 246-254; 426pp; English.

This sequence represents the wild-type L protein from Human parainfluenza virus (HPIV-3) type 3 isolate JS. This sequence is used in a method which involves the isolation of recombinantly-generated, attenuated, attenuated, attenuated and process of the sequence is used in a method which involves the isolation of recombinantly-generated.
                                                                                                                                                                                                                                                                                                                                  HPIV-3 JS isolate wild-type L protein.
L protein; attenuation; non-segmented; negative single stranded RNA virus; Mononegavirales.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibiting adhesion of T isolating agents to treat psoriasis, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BGHM ) BRIGHAM & WOMENS Brenner MB, Cepek KL; WPI; 95-392921/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-NOV-1995.
03-MAY-1995; U05518.
03-MAY-1994; US-237919.
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          involves the isolation of recombinantly-generated, attenuated, non-segmented, negative-sense, single stranded RNA virus of the order mononegavirales which have at least 1 attenuating mutation in the 3'
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151..702
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727..876
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Pred. No. 4.45e+01;
4; Mismatches 2;
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02-ARR-1998.
19-SEP-1997; U16718.
R 27-SEP-1996; US-026823.
A (AMCY ) AMERICAN CYANNAUD CO.
A (USSH) US DEFT HEALTH & HUMAN SERVICES.
PA (USSH) US DEFT HEALTH & SIdhu MS, Tatem JM
"""Thy BR, Randolph VB, Sidhu MS, Tatem JM
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L protein; attenuation; non-segmented; negative sense; vaccine; single stranded RNA virus; Mononegavirales.
Human parainfluenza virus.
W09813501-A2.
02-APR-1000
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W48713;
W48713;
13-OCT-1998 (firs
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27-SEP-1996; US-026823.
(AMCY) AMERICAN CYANAMID CO.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
MUIPHY BR, Randolph VB, Sidhu MS, Tatem
WPI; 98-230710/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinantly-generated, attenuated, non-segmented, negative-sense, single stranded RNA virus of order Mononegavirales - having attenuating mutation in 3' genomic promoter region and RNA polymerase gene, useful as vaccine to immunise against such virus Disclosure; page 265-273; 426pp; English.

This sequence represents the Human parainfluenza virus (HPIV-3) type 3 vaccine FRhl cp45 I protein. This sequence is used in a method which involves the isolation of recombinantly-generated, attenuated, non-segmented, negative-sense, single stranded RNA virus of the order Mononegavirales which have at least 1 attenuating mutation in the RNZ genomic promoter region and at least 1 attenuating mutation in the RNZ genomic promoter region and at least 1 attenuating mutation in the RNZ genomic promoter region and at least 1 attenuating mutation in the RNZ genomic promoter region and at least 1 attenuating mutation in the RNZ genomic promoter region and at least 1 attenuating mutation in the RNZ genomic promoter region and at least 1 attenuating mutation in the RNZ genomic promoter region and at least 1 attenuating mutation in the RNZ genomic promoter region and at least 1 attenuating mutation in the RNZ genomic promoter region and at least 1 attenuating mutation in the RNZ genomic promoter region and at least 1 attenuating mutation in the RNZ genomic promoter region and at least 1 attenuating mutation in the RNZ genomic promoter region and at least 2 attenuating mutation in the RNZ genomic promoter region and at least 3 attenuating mutation in the RNZ genomic promoter region and at least 3 attenuating mutation in the RNZ genomic promoter region and at least 3 attenuating mutation in the RNZ genomic promoter region and at least 3 attenuating mutation in the RNZ genomic promoter region and at least 3 attenuating mutation in the RNZ genomic promoter region and at least 3 attenuating mutation in the RNZ genomic promoter region and at least 3 attenuating mutation in the RNZ genomic promoter region and at least 3 attenuating mutatio
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N-PSDB; V18273\.
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Recombinantly-generated, single stranded RNA virus
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Protein; attenuation; non-segmented; negative sense;
ingle stranded RNA virus; Mononegavirales.
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2233 AA;
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2233 AA;
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  i, non-segmented,
Mononegavirales
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PT polymerase gene, useful as vaccine to immunise against such virus PS Disclosure; Page 283-291; 426pp; English.

CC This sequence represents the Human parainfluenza virus (HPIV-3) type 3 CC vaccine Vero cp45 L protein. This sequence is used in a method which CC involves the isolation of recombinantly-generated, attenuated, CC non-segmented, negative-sense, single stranded RNA virus of the order CC Mononegavirales which have at least 1 attenuating mutation in the 3' CC genomic promoter region and at least 1 attenuating mutation in the RNA CC polymerase gene. This RNA virus can be used as a vaccine to immunise an CC individual against such a virus.
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W82841:
W82841;
J05199882-A.
10-AUG-1993.
24-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUCEP-1 protein having neuron function activating activity for treating ischaemic brain diseases and nerve denaturation conditions such as Parkinson's and Alzheimer's diseases Claim 1; Fig 4; 17pp; Japanese.

The present sequence represents human cerebral protein-1 (HUCEP-1 has neuron function activating activity. HUCEP-1 is ufor treating ischaemic brain diseases and nerve denaturation conditions such as Parkinson's and Alzheimer's diseases. Sequence 456 AA;
                                                                                                                                                                                                                                                                             R40843 standard; Pro
R40843;
24-FEB-1994 (first
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19-MAR-1997; 065716.
19-MAR-1997; JP-065716.
                                                                                                                                                                                                       Bilirubin oxidase.
Bilirubin; oxidase; analytical;
polymerase chain reaction.
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                                                                                            protein
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larity 54.5%;
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PR 24-JAN-1992; JP-034126.

PA (AMAN) AMANO PHARM KK.

DR WPP; 93-284681/36.

DR WPPSDB; 047790.

PT culturing bilirubin oxidase prepn. useful as an analytical enzyme - by PT culturing bilirubin oxidase in transformant culture

PS Claim I; Page 29-32; 32pp; Japanese.

CC The sequence encodes bilirubin oxidase. The protein produced has a CC 38 amino acid signal peptide which is removed to give the mature CC protein (R40843).

SQ Sequence 572 AA;

Query Match 572; AB; Score 49; DB 8; Length 572; Best Local Similarity 13.3%; Pred. No. 1.57e+02; Matches 2; Conservative 12; Mismatches 1; Indels 0; Gaps 0; DB 282 idtrlpfkviasdsg 296

INSKIAFKIVSOEPA 15
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Search completed: Fri Jun 11 17:29:04 1999 Job time: 106 secs.

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

ıäbular output not generated. Fri Jun 11 17:25:31 1999; MasPar time 4.28 Seconds 140.445 Million cell updates/sec

Description: Perfect Score: Sequence: Title: >US-08-991-628-3 (1-15) from US08991628.pep 96 1 LNSKIAFKIVSQEPA 15

Scoring table: PAM 150 Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir60 1:pir1 2:pir2 3:pir3 4:pir4

Mean 25.594; Variance 33.108; scale 0.773

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22222296544322322222222233333333333333333333333	Result
55333444455555555555555555555555555555	Score
100 900 600 600 500 500 500 500 500 500 500 5	Query Match
999 1043 11049 11117 1421 884 884 886 906 385 1385 1385 1364 11264 1264 1264 1264 1264 1264 1264 1	Length
2112312122222222	8
IJHUG3 IJHUG1 S38673 ITO2501 ITO2501 IJHUCN S49752 S74520 S64116 IJFCTM F70126 IJFCTM F70126 IJFCTM F70126 IJFCTM F70126 IJFCTM F70126 IJFCTM IJHUCE S43064 IJHUCE IJHUCE S43064 IJHUCE	Ħ
desmoglein 3 precurso desmoglein 1 precurso desmoglein 2 - human desmoglein 2 - human hypothetical protein E-cadherin precursor uvomorulin - mouse cadherin 2 precursor hypothetical protein YOX1 hypothetical protein probable membrane procadherin related tumo translation elongatio N-cadherin precursor cadherin precursor probable transcriptio genome polyprotein - genome polyprotein - genome polyprotein - probable transcriptio	Description
2.05e-09 3.51e-07 3.51e-07 8.47e-05 2.82e-01 4.53e-01 4.53e-01 1.15e+00 1.81e+00 6.93e+00 6.90e+00 6.90e+00 6.9	Pred. No.

Query Match 100.0%; Best Local Similarity 100.0%; Matches 15; Conservative

Score 96; DB 1; Length 999; Pred. No. 2.05e-09; 0; Mismatches 0; Indels

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Gaps

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Bombyx mor1 receptor	plastoquinolplastoc	probable GMP synthase	genome polyprotein 1	genome polyprotein 1	hypothetical protein	hypothetical protein	sodium/pantothenate s	carbonyl reductase (N	carbonyl reductase (N	antibiotic resistance	aspartic proteinase i	beta 8 integrin - chi	ribosomal-protein-ala	hypothetical protein	isocitrate dehydrogen	hetical pro	protein -	protein -	ribosomal protein S3	calpain (EC 3.4.22.17	B-caunerin precursor
5.75e+01	5.75e+01	5.75e+01	3.81e+01	3.81e+01	3.81e+01	3.81e+01	٠	•	٠	3.81e+01		3.81e+01	3.81e+01	2.51e+0	2.51e+01	2.51e+01	2.51e+01	2.51e+01	2.51e+01	1.65e+01	T. ODETOI

ALIGNMENTS

SUMMARY	910-938 937-966 110,180,545	616-639 640-999	270-383 390-495	52-157 160-267	50-615	70-999	FEATURE	REXECUTE	#map_position CLASSIFICATION	##cross-rel	#gene	GENETICS	##cross-references	##molecule_type mRNA	#accession	#cross-referer	#title	#journal	#authors	ACCESSIONS	DATE	ALTERNATE_NAMES ORGANISM	TITLE	RESULT 1
#length 999 #molecular-weight 107502 #checksum 8311	<pre>#domain desmoglein repeat #label DG1\ #domain desmoglein repeat #label DG2\ #binding_site carbohydrate (Asn) (covalent) #status</pre>	#domain transmembrane #status predicted #label IMM\ #domain intracellular #status predicted #label IMM\	cadherin repeat homology #label cadherin repeat homology #label	cadherin repeat homology #label cadherin repeat homology #label	MAT\ #domain extracellular #status predicted #label EXT\	#UDMMAIN PROPERTIES TO THE TRANSPORT OF	11.0 R+(10+1	catcium pinding; cett adnesion; dupitcation; giycopiotein;		##cross-references GDB:134030; OMIM:169615	GDB: DSG3		GB:M76482;	type mrnA 1-999 ##1abel AMA	A41088	pemphigus vulgaris, a disease of cell adhesion. #cross-references MUID:92069753		91) 67:869-877	Amaga: M.: Klaus-Kovtun, V.: Stanlev, J.R.	A41088	<pre>30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 18-Sep-1998</pre>	pemphigus vulgaris antigen #formal_name Homo sapiens #common_name man	desmoglein 3 precursor - human	TIUTIC3 #+vno complete

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#gene
CLASSIFICATION
KEYWORDS
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**cross-references GB:S64268; GB:S64270

REFERENCE A37785
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##cross-references EMBL:X57784; NID:g436061; PID:g436062
**NCE A48173
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##residues 44-1001,'AQPPSAT' ##label KO3
##cross-references GB:X57784
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##cross-references GB:M58165; NID:g162966;
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submitted to the EMBL Data Library, March 1991
Complete sequence of the desmoglein precursor and evidence
for the existence of different desmoglein genes expressed
in cell type-specific patterns.
                                                                                                                                                                                                                                                                                                                                              Koch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zimbelmann, R. submitted to the EMBL Data Library, February 1991 $38721
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Blochem. Blophys. Res. Commun. (1990) 173:1224-1230
          #superfamily cadherin; cadherin repeat homology
calcium binding; cell adhesion; duplication; glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goodwin, L.; Hill, J.E.; Raynor, K.; Raszi, L.; Manabe,
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desmoglein 1 precursor - bovine
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                                                                                                                                                                                                                                            glycoprotein, as a member of the cadherin adhesion molecules.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell Biol. (1991) 55:200-208
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                                                                                                                                              Wagner, R.M.; Green, K.J.
J. Cell Sci. (1991) 99:809-821
Structural analysis and expression
Structural component of the de
Wheeler, G.N.; Buxton, R.S.; Parker, A.E. Rees, D.A.; King, I.A.; Magee, A.I. Blochem. Soc. Trans. (1991) 19:1060-1064 Desmosomal glycoproteins I, II and III:
                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. (1991) 88:4796-4800 Desmosomal glycoprotein DGI, a component of interc desmosome junctions, is related to the cadherin
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#formal_name Homo sapiens #common_name man
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#map_position 18q12.1-18q12.2
CLASSIFICATION #superfamily cadherin; cadherin
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##molecule_type mRNA
777-1117 ##label KOC
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##residues 1-1117 ##label ZIM
##cross-reference EMBL:Z26317; NID:g416177; PID:g416178
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##residues 1-55 ##label WH3
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calcium binding; cell adhesion; duplication; glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                            Zimbelmann, R.
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                                                                                              precursor polypeptide and identification of a second type of desmoglein gene.
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##molecule_type mRNA
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1-412,'V',414-884 ##label NAG
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p_position 18q12.1-18q12.2
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Similarity 73.3%;
11; Conservative
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E-cadherin precursor, epithelial - mouse
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calcium binding; cell adhesion; duplication; glycoprotein;
                                                                    Transformation of cell adhesion introduced E-cadherin cDNA. ccs_MUID:87315445
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30-Jun-1993 *sequence_revision 30-Jun-1993 *text_change
13-Mar-1997
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                                                                                                                              Nature (1987) 329:341-343
                                                                                                                                                                Nagafuchi, A.; Shirayoshi, Y.; Okazaki,
                                                                                                                                                                                                        S04528; S03160; I49565; S48735
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#domain cadherin repeat homology #label CR2
yth 1117 #molecular-weight 122384 #checksum
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Pred. No. 8.47e-05;
3; Mismatches 1
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Best Local Similarity
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#cross-references MUID:92107977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #title Purification and spectroscopic characterization of a recombinant amino-terminal polypeptide fragment of epithelial cadherin.
#cross-references_MUID:95010732
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#accession S03160
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299 NAAIAYTIVSQDP 311
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##residues 156-300 ##label TON
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##cross-references EMBL:X06339
##note part of this sequence,
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Lottspeich, F.; Engel, J.; Doelz, R.; Jaehnig, F.; E
J.; Mayer, S.; Mueller, C.; Kemler, R.
EMBO J. (1987) 6:3647-3653
The structure of cell adhesion molecule uyomorulin. In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #superfamily cadherin; cadherin repeat homology
calcium binding; cell adhesion; duplication; glycoprotein;
transmembrane protein
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The B-cadherin promoter: Functional analysis of a G-C-rich
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larity 61.5%;
Conservative
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#product E-cadherin, epithelial #status experimental
#label MAT\
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4.53e-01;
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                                                                                     #authors
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##note the nucleotide sequence was
Library, August 1992
                                                                                                                  ##cross-references EMBL:X54315
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NCE S11487
                                                                                                                                                                                                                                                                                                                ##molecule_type mRNA
##residues 1-906 ##label REI
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##residues 1-884 ##label RIN
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1-340,'N',342-698,'R',700-704,'F',706-906 ##label RE2
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Similarity 61.5%;
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Nucleic Acids Res. (19
Human N-cadherin: nuc
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The structure of the gene coding for the mouse cell
                                D.; Spurr, N.; Goodfellow, P.
J. Neurochem. (1990) 55:805-812
N-cadherin gene maps to human c
                                                                                                     JQ0751
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submitted to the EMBL Data Library, November
                                                                                                                                                                                                                                                                                                                                                                                                                    A38870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    #formal_name Homo sapiens #common_name man 30-Jun-1993 #sequence_revision 30-Jun-1993
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N-cadherin; neuronal cadherin
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#length 884 #molecular-weight 98283
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                                                                                   Walsh, F.S.; Barton, C.H.; Putt, W.;
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to the E-cadherin gene
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Pred. No. 4.53e-01
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(1990) 18:5896
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                                                                                     Moore, S.E.;
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##molecule_type mRNA
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##cross-references SGD:S0004489; MIPS:YML027w
#map_position 13L
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                                                                                                                                                                           #cross-references
                                                                                                                                                                                                                                                            #authors
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;72,622,651,692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##cross-references GB:M34064
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                                                                                                             ##residues
                                                                                                                             ##molecule_type DNA
                                                                                                                                                                                                                                                                                                  ##residues 1-385 ##label BAD
##cross-references EMBL:246659; NID:g575680;
                                                                                                                                                                                                                                                                                                                                              ##molecule_type DNA
                                                                                         ##cross-references
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LNSKIAFKIVSQEPA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 62.5%;
Similarity 46.7%;
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               $49752  #type complete
homeotic protein YOX1 - yeast (Saccharomyces cerevisiae)
protein YML027w
#formal_name Saccharomyces cerevisiae
13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change
                                                                                                                                                                                             Chromosoma (1993) 102:174-179
In vitro binding to the leucine
yeast homeobox gene.
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calcium binding; cell adhesion; duplication; glycoprotein;
                                                                                                                                                                                                                                                                Kaufmann, E.
                                                                                                                                                                                                                                                                                                                                                                           S49752
                                                                                                                                                                                                                                                                                                                                                                                           Badcock, K.; Churcher, C. submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #length
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                                                                                    1-290,'QGLIIP' ##label KAU
es EMBL:X62392; NID:g5501;
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#domain cadherin repeat homology *label CR1\
*region cadherin binding *status predicted\
#domain cadherin repeat homology *label CR2\
#domain cadherin repeat homology *label CR3\
#domain cadherin repeat homology *label CR3\
#domain cadherin repeat homology *label CR5\
#domain cadherin repeat homology *label CR5\
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#product N-cadherin #status predicted #label MAT\
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Pred. No. 4.53e-01
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#title
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PID:g1651744
##molecule_type
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similarity 38.5%;
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Similarity 63.6%;
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                                                                                                   hypothetical protein G2842
#formal_name Saccharomyces cerevisiae
17-May-1996 #sequence_revision 17-May-1996
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DNA Res. (1996) 3:109-136
Sequence analysis of the genome of the unicellular
cyanobacterium Synechocystis sp. PCC6803. II. Sequence
determination of the entire genome and assignment of
                                                                                                                                                 S64146 #type complete probable membrane protein cerevisiae)
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                            submitted to the
                                                                       S64146; S71739
                                                                                                                                                                                                                                                                                                                                                                   #superfamily hypothetical protein s1r0725
#length 138 #molecular-weight 16580 #ch
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Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.;
Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;
Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shim
S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
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6803)
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                                                                                       7-Apr-1998
                                                                                                                                                                                                                                                                                                                                                                                                                             the nucleotide sequence was submitted to Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid sequence not shown; translation not shown
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                         Eraso, P.;
he Protein
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Pred. No. 1.15e+00;
7; Mismatches 1
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                               Database,
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                                                                                                                                                                   yeast
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                              Mazon, M.J.
ase, May 1996
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Best Local Similarity 42.9%;
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51-156
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##cross-references GB:M80537
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##cross-references EMBL:X9260
the nucleotide sequence
##note Library, October 1995
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##cross-references GB:M80537
                                                                                                                                                                                                                                                                                                                   ##molecule_type DNA
                                                                                                                                               ##cross-references FlyBase:FBgn0001075
FICATION #superfamily cadherin-related tumor suppressor; cadherin repeat homology; EgF homology
DS calcium binding; cell adhesion; duplication; transmembrar
                                                                                                                                                                                                                                                                  ##note
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                                                                                                                                                                                                                                                                                                                                            B41087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Drosophila melanogaster)
#formal_name Drosophila melanogaster
30-Sep-1993 #sequence_revision 30-Sep
16-Feb-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   The fat tumor suppressor gene in Drosophila encodes member of the cadherin gene superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bryant, P.J.; Goodman, C.S. Cell (1991) 67:853-868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IJFFTM #type complete cadherin-related tumor suppressor precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transmembrane protein
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MUID:96437978
#domain extracellular #status predicted #label EXT\
#domain cadherin repeat homology #label CR1\
#domain cadherin repeat homology #label CR2\
                                                        #product cadherin-related tumor
predicted #label MAT\
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Pred. No. 1.81e+00;
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#cross-references MU
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                      Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.;
Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.;
Dodson, R.; Hickey, E.K.; Gwinn, M.; Dougherty, B.; Tomb,
J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.;
Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.;
Vugt, R. V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weidman,
J.; Utterback, T.; Watthey, L.; McDonald, L.; Artiach, P.;
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst,
K.; Roberts, K.; Hatch, B.; Smith, H.O.; Venter, J.C.
Nature (1997) 390:580-586
Genomic sequence of a Lyme disease spirochaete, Borrelia
burgdorferi.
                                                                                                                                                                                                                                                spirochete
formal_name Borrelia burgdorferi #common_name Lyme disease
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                                       271 LNGMLRYRILSQAPS 285
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##cross-references EMBL:X53615; NID:g164; PID:g664894
##Cadherins mediate calcium-dependent intercellular adhesion, and
thought to be involved in the sorting of different cell types
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calcium binding; cell adhesion; duplication; glycoprotein;
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N-cadherin precursor - bovine (fragment)
#formal_name Bos primigenius taurus #common_name cattle
30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
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:es GB:AE001132; GB:AE000783; NID:g2688107; PID:g2688116;
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Pred. No. 4.46e+00;
3; Mismatches 4
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Pred. No. 6.93e+00;
7; Mismatches 2
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RESULT ENTRY

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#type complete

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##residues 1-882 ##label BUS
##cross-references EMBL:Z13009; NID:g31072; PID:g31073
REFERENCE S31430
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                                                              #authors #journal
                                                                                                                                                                                                                                                                                                     #journal
#title
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#journal Differentiation (1988) 38:67-71

#title Characterization and chromosomal localization of the gene

#title encoding the human cell adhesion molecule uvomorulin.

#cross-references MUID:89031725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #journal
#title
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#cross-references MUID:95324920
#accession A57171
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##cross-references EMBL:Z18923; NID:g31074;
                                                                                                                            ##cross-references GB:L34784
                                                                                                                                                     ##residues
                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type protein
##residues 'XQ',157-162,'V',164-179 ##label WHE
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##residues 265-392 ##label FRI
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##residues 157-311 ##label MAN
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Genomics (1995) 26:281-289
Cloning and characterization of the I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birchmeier, W.
submitted to the EMBL Data Library,
Sequence of human E-cadherin cDNA.
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ARC-1; cell CAM 120/80; E-cadherin; epithelial cadherin;
Rimm, D.L.; Morrow, J.S.
Biochem. Biophys. Res. Commun. (1994) 200:1754-1761
Molecular cloning of human E-cadherin suggests a nov
subdivision of the cadherin superfamily.
nces MUID:94242050
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Mol. Biol. Rep. (1993) 17:123-128
Molecular cloning and characterization of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Cell. Biochem. (1987) 34:187-202
Soluble 80-kd fragment of cell-CAM 120/80 disrupts cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Frixen, U.H. submitted to the EMBL Data Library, March 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kelker, W.; Warda, A.; Oda, T.; Hirohashi, S.; Kemler,
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                                                                                                                                                                                                                                                                                                                                                                   Berx, G.; Staes, K.; van Hengel, J.;
                                                                                                                                                                                                                                                                                                                                                                                            A57171
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30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
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                                                                                                                                                                                                                   nucleic acid
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                                            novel
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REFERENCE

##molecule_type DNA ##rresidues 1-16 ##label RES ##cross-references GB:L34545; NID:g509604; PID:g509605 NCE 152704

translation not shown; translated from GB/EMBL/DDBJ

Becker, K.F.; Atkinson,

M.J.; Reich, U.; Becker, I.; Nekarda,

#journal #authors REFERENCE

##note

##cross-references GB:L08599;

pes GB:L08599; NID:g340184; PID:g340185 the majority of differences between this and other reports represent apparant frameshift errors the authors translated the codon CCG for residue 868

,11-15,'RSPLGSQERSPPPCLTRELHVHGAPAPPEKRPR',52-67,9,'LTPIP',76-94,'TDP',98-99,'GLR',103-482,'G',29,'R',531-614,'H',616-633,'RVP',637-867,'P',

##molecule_type mRNA ##residues 1-9,

#authors

Schalken

#journal #title

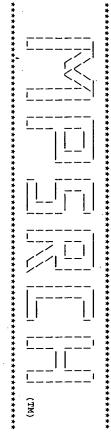
Biochem. Biophys. Res. Commun. (1994) 203:1284-1290 Transcriptional regulation of the human E-cadherin gene human prostate cancer cell lines.

Bussemakers, M.J.G.; Giroldi, L.A.; van Bokhoven, A.;

#cross-references MUID:94380041

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                                                                                                                                       Query Match
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                                           297 NAAIAYTILSODP 309
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T Cadherins mediate calcium-dependent intercellular adhesion and are
thought to be involved in the sorting of different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #molecule_type DNA
                                                                                    Match 56.3%;
Local Similarity 53.8%;
local 7; Conservative
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Cancer Res. (1994) 54:3845-3852
E-cadherin gene mutations provide clues to diffuse type gastric carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *superfamily cadherin; cadherin repeat homology calcium binding; cell adhesion; duplication; glycoprotein; transmembrane protein
                                                                                                                                                                            predicted
#length 882 #molecular-weight 97455 #checksum 5112
                                                                                                                                                                                                                          #binding_site carbohydrate (Asn)
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#domain propeptide #status predicted #label PRO\
#product E-cadherin #status experimental #label MAT\
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domain cadherin repeat homology *label CRI
region cadherin binding *status predicted
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Search completed: Fri Jun 11 17:26:59 1999 Job time: 88 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:22:45 1999; MasPar time 2.44 Seconds 173.855 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-991-628-3 (1-15) from US08991628.pep 96

LNSKIAFKIVSQEPA 15

Scoring table: PAM 150 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot37 1:swissprot

Statistics: Mean 26.281; Variance 28.608; scale 0.919

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	RETINAL-CADHERIN PRECU	RETINAL-CADHERIN PRECU	NEURAL-CADHERIN 1 PREC	HYPOTHETICAL 67.5 KD P	BILIRUBIN OXIDASE PREC	APOCYTOCHROME F PRECUR	APOCYTOCHROME F PRECUR	ACYL TRANSFERASE (EC 2	RRNA ADENINE N-6-METHY	GENOME POLYPROTEIN 1 [GENOME POLYPROTEIN 1 [TRANSITIONAL ENDOPLASM	VACB PROTEIN.	PROBABLE METHYLTRANSFE	CARBONYL REDUCTASE [NA	ASPARTIC PROTEINASE IN	ISOCITRATE DEHYDROGENA	HYPOTHETICAL 74.5 KD P	SURFACE PRESENTATION O	CALPAIN P94, LARGE [CA	`
1.96e+01	1.96e+01	1.96e+01	1.96e+01	1.96e+01	1.96e+01	1.96e+01	1.96e+01	1.96e+01	1.96e+01	1.23e+01	1.23e+01	1.23e+01	1.23e+01	1.23e+01	1.23e+01	1.23e+01	7.62e+00		7.62e+00	4.69e+00	4.69e+00

ALIGNMENTS

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EMBL; M76482; G190752; PIR; A41088; IJHUG3. MIM; 169615; PROSITE; PS00232; CADHERIN; 3. PFAM; PF00028; cadherin; 4. HSSP; P09803; 1EDH.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).	(POTENTIAL). (POTENTIAL). (POTENTIAL) (PO	MEDLINE; 92069753. MEDLINE; 92069753. MANAGAI M., KLAUS-KOVTUN V., STANLEY J.R.; ANAGAI M., KLAUS-KOVTUN V., STANLEY J.R.; "AUTOANTIONCIONE SPACINIST A DOVEL EPITHEIIAL CACHEIN IN PEMPHIGUS VULGATIS, A disease of cell adhesion."; CELL 57:869-877(1991). -!- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. -!- FUNCTION: COMPONENT OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION. -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. -!- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL, OESOPHAGUS AND CARCINOMAS.	3 PRECURSOR S (HUMAN). METAZOA; CH ATARRHINI;	LT 1 DSG3_HUMAN STANDARD; PRT; 999 AA. p32926; p1-0CT-1993 (REL. 27, CREATED) O1-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE) O1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

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REPEAT
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                                                                                                                                                                                               MEDLINE: 92
KOCH P.J.,
                                                                                                                                                                                                                                                                                                                                                                      (1)
SEQUENCE FROM N.A.
TISSUE-MUZZLE EPITHELIUM;
KOCH P.J., GOLDSCHMIDT M.D., ZIMBELMANN R., FRANKE W.
KOCH P.J., MAR-1991) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSG1_BO
Q03763;
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01-OCT-1993 (REL. 27,
01-NOV-1997 (REL. 35,
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GOODWIN L., HILL J.E., RAYNOR K., RASZI L., MANABE "Desmoglein shows extensive homology to the cadheri adhesion molecules.";
BIOCHEM. BIOPHYS. RES. COMMUN. 173:1224-1230(1990).
-!- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS FILAMENTS MEDIATING CELL-CELL ADHESION.
                                                                                                                                                                                                                                                                glycoprotein, as a member of the molecules.";
                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 44-1043 FROM N.A. TISSUE-MUZZLE EPITHELIUM; MEDLINE; 91168965.
                                                                                                                                         polypeptide and EUR. J. CELL BIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA;
                                                                                               SEQUENCE OF 44-493 FROM N.A. MEDLINE; 91097553.
                                                                                                                                                   PARAMA THE PROPERTY OF THE PRO
                                                                                                                                                                                  FRANKE W.W.;
                                                                                                                                                                                                                             REVISIONS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 LNSKIAFKIVSQEPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ۲
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ARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
PECORA; BOVOIDEA; BOVIDAE;
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Similarity 100.0%;
15; Conservative
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                                                                                                                                         identification of a second DL. 55:200-208(1991).
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                          SCHMELZ M.,
                                                                                                                                                                                                                             101-123
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Pred. No. 1.36e-11
0; Mismatches
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                                                                   MANABE M.
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EMBL; X58466; G307; -.
EMBL; X57784; G436062; -.
EMBL; M58165; G552318; -.
PIR: S14603; JIBOG1.
PROSITE; PS00232; CADHERIN; 2
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HSSP; P09803; 1EDH.
CELL ADHESION; SIGNA
CALCIUM-BINDING; REF
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01-OCT-1993
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- TISSUE SPECIFICITY: EPIDERMIS, MUZZLE, TONGUE AND
-i- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
ARNEMANN J., RUTMAN A.J. BUXTON R.S., MAGEE A.I.;
                TISSUE-KERATINOCYTES;
MEDLINE; 91271279,
WHEELER G.N., PARKER A.E.,
ARNEMANN J., RUTMAN A.J.,
                                                                                                                                                     01-0CT-1993 (REL. 27, C
01-0CT-1993 (REL. 27, L
01-NOV-1997 (REL. 35, L
DESMOGLEIN 1 PRECURSOR
                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                               DSG1_HUMAN
Q02413;
                                                                      SEQUENCE FROM N.A
                                                                                                 PRIMATES; CATARRHINI;
                                                                                                                                                                                                                                                                                                    190 LNSKIAFKIIRQEPS 204
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SIMILARITY: BELONGS TO
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27, LAST SEQUENCE UPDATE)
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URSOR (DESMOSOMAL GLYCOPROTEIN 1)
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                 , THOMAS
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Pred. No. 5:65e-09;
2; Mismatches 1
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POTENTIAL.
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MW; 13898584 CRC32;
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                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                            01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DESMOGLEIN 2 PRECURSOR (HDGC).
                                                                                                          DSG2_HUMAN
Q14126;
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REPEAT
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HSSP; P09803; 1EDH
CELL ADHESION; SIGN
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MIM; 125670; -.
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                                                                                                                                                                                                        Local Similarity nes 12; Conser
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FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS.
INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDI
FILAMENTS MEDIATING CELL-CELL ADHESION.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSILAND OESOPHAGUS.
DOMAIN: CRACCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
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SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                              LNSKIAFKIVSQEPA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00232; CADHERIN;
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the cadherin family
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Pred. No. !
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DESMOGLEIN REPEAT 2.
DESMOGLEIN REPEAT 3.
DESMOGLEIN REPEAT 4.
DESMOGLEIN REPEAT 5.
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5.65e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUR. J. CELL BIOL. 55:200-208(1991).

-I- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUN INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND FILAMENTS MEDIATING CELL-CELL ADHESION.

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY -I- TISSUE SPECIFICITY: ALL OF THE TISSUES TESTED AND -I- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KOCH P.J., GOLDSCHMIDT M.D., WALSH M.J., ZIMBELMANN R., FRANKE W.W.; "Complete amino acid sequence of the epidermal desmoglein precursor polypeptide and identification of a second type of desmoglein gene."; EUR. J. CELL BIOL. 55:200-208(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCHAEFER S., KOCH P.J., FRANKE W.W.;
"Identification of the ubiquitous human desmoglein, Dsg2, and the expression catalogue of the desmoglein subfamily of desmosomal cadherins.";
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HSSP; P15116; INCI
CELL ADHESION; GLY
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                              191 LNSKISYRIVSLEPA 205
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SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS TO THE DESMOSOMAL SUBFAMILY.
LNSKIAFKIVSQEPA
                                                           Similarity 73.3% 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CALCIUM-BINDING
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48
1117
608
633
1117
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                                                          Score 77; DB 1; 1
Pred. No. 3.44e-06;
3; Mismatches 1
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DESMOGLEIN
DESMOGLEIN
POTENTIAL.
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CADHERIN
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DESMOGLEIN
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EXTRACELLULAR
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AND INTERMEDIATE
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CARCINOMAS.
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01-MAR-1989 (REL. 10, 0
01-MAR-1989 (REL. 10, 1
15-JUL-1998 (REL. 36, 1
EPITHELIAL-CADHERIN PRI
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01-MAR-1989 (REL.
01-MAR-1989 (REL.
15-JUL-1998 (REL.
                                                                                                                                                                                                                                            OVERDUIN M., TONG K.I., KAY C.M., IKURA M.;

"1H, 15N and 13C resonance assignments and monomeric structure of the manino-terminal extracellular domain of epithelial cadherin.";

J. BIOMOL. NMR 7:173-189(1996).

-i- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS. THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 92107977.
BEHRENS J., LOEWRICK O., KLEIN-HITPASS L., BIRCHMEIER W.;
"The E-cadherin promoter: functional analysis of a G.C-rich region and an epithelial cell-specific palindromic regulatory element.";
PROC. NATL. ACAD. SCI. U.S.A. 88:11495-11499(1991).
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NAGAR B., OVERDUIN M., IKURA M., RINI J.M.;
"Structural basis of calcium-induced E-cadherin rigidification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The structure of cell adhesion molecule uvomorulin. Insights into the molecular mechanism of Ca2+-dependent cell adhesion."; EMBO J. 6:3647-3653(1987).
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RINGWALD M., SCHUH R., VESTWEBER D., EISTETTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            molecule uvomorulin.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                 This
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"The structure of the gene
                                                                                            the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 157-370.
                                                                                                                                                          SORTING OF HETEROGENEOUS CELL TYPES.
SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: NON-NEURAL EPITHELIAL TISSUES.
SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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G50765;
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JAEHNIG F., EPPL
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), LAST SEQUENCE UPDATE)
5, LAST ANNOTATION UPDATE)
PRECURSOR (E-CADHERIN) (UVOMORULIN) (ARC-1)
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EPPLEN J., MAYER S.,
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P19022; 014923;
01-NOV-1990 (REL. 16, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
CDH2 OR CDHN OR NCAD.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTPRIMATES; CATARRHINI; HOMINIDAE; HOMO.
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EMBL;
                                   NUCLEIC ACIDS
[2]
                                             REID R.A., HEMPERLY J.J.;
"Human N-cadherin: nucleotide and dedu
NUCLEIC ACIDS RES. 18:5896-5896(1990).
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PFAM; PF01049; Cadherin_C_term;
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PROSITE; PS00232; CADHERIN;
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EMBL; M81449;
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 REID R.A.;
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                   699 AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         re 60; DB 1; Len d. No. 7.44e-02; Mismatches 2;
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REF. 2).
CRC32;
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                                                                    amino
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                                                                 acid sequence.";
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EMBL; X57548; E31840; -.
EMBL; X54315; G34999; -.
EMBL; X2303; G253483; -.
EMBL; M34064; G416293; -.
EMBL; 227420; G806346; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WALLIS J.A., FUX M., PALLING THE WALLIS J.A., FUX M., PALLING THE WALLIS J.A., FUX M., PALLING THE WALLING THE WAL
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WALLIS J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBMITTED
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PROPEP
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SPURR N., GOODFELLOW P.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as modified and this statement is not removed. U entitles requires a license agreement (See htt or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF01049; Cadherin_C_term;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIN.
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MEDLINE; 92363956.
SALOMON D., AYALON O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "N-cadherin gene maps to 
E-cadherin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SORTING OF HETEROGENEOUS CELL TYPES. NEURONAL RECOGNITION MECHANISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A38870; IJHUCN.
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90347462.
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    FROM N.A
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CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
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CYTOPLASMIC
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EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
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       3 AND
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01-OCT-1996
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P34161;
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
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                                                                           DNA_BIND
                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                    EMBL; X62392; G5502; -.
EMBL; Z46659; G575692; -.
PIR; S33388; S33388.
SGD; L0002540; YOX1.
                                                                                                                                                                                                                                                                                                                                BADCOCK K., CHURCHER C., BARRELL B.G., RAJANDREAM M.A., WALSH SUBMITTED (NOV-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- FUNCTION: IN VITRO, IS CAPABLE OF BINDING TO THE DNA OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                           PFAM; PF00046
HSSP; P06601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O1-FEB-1994 (REL. 28, CREATED)
O1-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
O1-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HOMEOBOX PROTEIN YOX1.
                                                                                                                               PROSITE; PS00027; PROSITE; PS50071;
                                                                                                                                                                                                                                                                                                                                                                  STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                  CHROMOSOMA 102:174-179(1993).
                                                                                                                                                                                                                                                                                                                                                                                                             homeobox gene.
                                                                                                                                                                                                                                                                                                                                                                                                                  "In vitro binding to the leucine tRNA gene identifies
                                                                                                                                                                                                                                                                                                                                                                                                                                   KAUFMANN E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-296 FROM N.A.
                                                                                                 HOMEOBOX;
                                                                                                                                                                                                                                                                                                  -1- SIMILARITY: WITH OTHER HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOX1 OR YML027W
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364 KFGFKIVDQQP 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LNSKIAFKIVSQEPA 15
                                                                                                                                                                                                                                                                                                          LEUCINE TRNA GENE.
SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                      PF00046;
                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 46.7% 7; Conservative
                                                                                                                              PS00027; HOMEOBOX_1;
PS50071; HOMEOBOX_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                              93209080
                                                                                                DNA-BINDING; NUCLEAR PROTEIN.
                                                               291
385 AA;
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212
357
867
906
                     Conservative
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42739
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212
357
867
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46.7%;
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PRPHHS -> QGLIIP
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                     re 59; DB 1; I
1. No. 1.28e-01;
Mismatches 1
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1. No. 7.44e-02;
1. no. ---hes 2;
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REF. 4
REF. 1
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CRC32;
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                                           Length 385;
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                                                                                        "The fat tumor suppressor gene in Drosophila encodes a novel membe of the cadherin gene superfamily.";
CLLL 67:853-868 (1991).
-i- FUNCTION: COULD FUNCTION AS A CELL-ADHESION PROTEIN.
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- DISEASE; RECESSIVE LETHAL MUTATIONS IN FAT CAUSE HYPERPLASTIC,
TUMOR-LIKE OVERGROWTH OF LARVAL IMAGINAL DISCS, DEFECTS IN
DIFFERNTIATION AND MORPHOGENESIS, AND DEAT DURING THE PUPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-5288C / FY1679;
STRAIN-5288C / FY1679;
MEDLINE; 96437978.
MEDLINE; 96437978.
ESCRIBANO V., ERASO P., PORTILLO F., MAZON M.J.;
"Sequence analysis of a 14.6 kb DNA fragment of Saccharomyces "Sequence analysis of a 14.6 kb DNA fragment of Saccharomyces cerevistae chromosome VII reveals SEC27, SSMIb, a putative S-adenosylmethionine-dependent enzyme and six new open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YGN3_YEAST STANDARD; PRT; 1264 AA.
P53125;
p53125;
01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-DEC-1996 (REL. 37, LAST ANNOTATION UPDATE)
HYPOTHETICAL 145.6 KD PROTEIN IN RPL1B-CEG1 INTERGENIC REGION.
YGL133W OR G2842.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                   DROSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
DROSOPHILIDAE; DROSOPHILA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAT_DROME P33450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z72655; E243361; -. HYPOTHETICAL PROTEIN. SEQUENCE 1264 AA; 1456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     frames.";
YEAST 12:887-892(1996).
   DIFFERENTIATION AND MORPHOGENESIS, AND DEAT DURSTRACE.
SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
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DOUGHRATY B., TOMB J.F., FLEISCHMANN R.D., RICHARDSON D.,
PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S.,
VAN VUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J.,
UTTERBACK T., WAITHEY L., MCDONALD L., AFTIACH P., BOWMAN C.,
GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                burgdorferi.";
NATURE 390:580-586(1997).
                                                                                                                                                                                                       EMBO
                                                                                                                                                                                                                        MEDLINE; 90360979.
LIAW C.W., CANNON C., POWER "Identification and cloning endothelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
NEUVAL-CADHERIN PRECURSOR (N-CADHERIN) (FRAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01275; EFP; FALSE_NEG.
PROTEIN BIOSYNTHESIS; ELONGATION FACTOR.
SEQUENCE 192 AA; 21413 MW; CB74964B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genomic sequence of a Lyme disease spirochaete,
                                                                                                                                                                                                                                                                                                                                     BOS TAURUS EUKARYOTA;
                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                      ARTIODACTYLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 LAPKIAFEVVEVEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LNSKIAFKIVSQEPA
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PATHWAY: PROTEIN BIOSYNTHESIS.

SIMILARITY: BELONGS TO THE ELONGATION FACTOR P FAMILY.
                                                                                         O J. 9:2701-2708(1990).
FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED I
NEURONAL RECOGNITION MECHANISM.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: INVOLVED IN PEPTIDE BOND SYNTHESIS. STIMULATE EFFICIENT TRANSLATION AND PEPTIDE-BOND SYNTHESIS ON NAMIVE OR RECONSTITUTED 70S RIBOSOMES IN VITRO. PROBABLY FUNCTIONS INDIRECTLY BY ALTERING THE AFFINITY OF THE RIBOSOME FOR AMINOACYL-TRNA, THUS INCREASING THEIR REACTIVITY AS ACCEPTORS FOR PEPTIDYL TRANSFERASE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BB0214;
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Similarity 53.3%;
8; Conservative
                                                                                                                                                                                                                                                                    FROM N.A.
90360979.
                                                                                                                                                                                                                                                                                                          (BOVINE).
METAZOA; CHORDATA; VERTEBRATA; MA
METAZOA; CHORDATA; PECORA; BOVOIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                  (REL.
(REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                        M.D., K
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Pred. No. 1.04e+00;
3; Mismatches 4
                                                                                                                                                                                                                                       KIBONEKA P.K., RUBIN L.L. o species of cadherins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      877
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A; BOVIDAE;
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SCHALKEN J.A.; rin gene in human the human E-cadherin

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Query Match
Best Local
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PIR; S11693;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                            CAD1_HUMAN STANDARD; PRT; 882 AA. P12830; Q14216; O1-OCT-1989 (REL. 12, CREATED) O1-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE) 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) EPITHELIAL-CADHERIN PRECURSOR (E-CADHERIN) (U
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CARBOHYD
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or send a
MEDLINE: 89031725.

MANSOURI A., SPURR N., GOODFELLOW P.N., KEMLER "Characterization and chromosomal localization the human cell adhesion molecule uvomorulin."; DIFFERENTIATION 38:67-71(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00232; CADHERIN;
                                                                                               SEQUENCE OF 172-311
                                                                                                                           SUBMITTED
                                                                                                                                        SEQUENCE FROM N.A. KELKER W., WARDA &
                                                                                                                                                                                                                         SCHALKEN J.A.;
                                                                                                                                                                                                                                    BUSSEMAKERS M.J.G.,
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE; 93211394.
                                                                                                                                                                                                                                                                                        CDH1 OR UVO OR CDHE.
HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271 LNGMLRYRILSQAPS
                                                                                                                                                                                                          Molecular cloning
                                                                                                                                                                                  BIOL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 56.3%;
Similarity 40.0%;
6; Conservative
                                                                                                                           (XXX-1992)
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                                                                                                                                                                                  REP.
                                                                                                                                         WARDA A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G664894; -.
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                                                                                                                                                                                17:123-128(1993)
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13
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                                                                                                                                                                                                            characterization
                                                                                                                                                                                                                                      S.G.M.,
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Pred. No. 1.
7; Mismatc
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CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
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SER-RICH.
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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1.74e+00;
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                                                                                                                         , KEMLER R., BIRCHMEIER W.;
DATA BANKS.
                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                               (UVOMORULIN) (CAM 120/80)
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                                        of 25
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                                         the gene encoding
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    VARIANTS ALA-370 AND ASN-473.

MEDLINE; 94306394.

BECKER K.-F., ATKINSON M.J., REICH
SIEWERT J.R., HOEFLER H.;

"E-cadherin gene mutations provide carcinomas.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANTS THR-617; VAL-711 AND GLY-838.

MEDLINE: 9435985.

RISINGER J.I., BERCHUCK A., KOHLER M.F., BOYD J.;

"Mutations of the E-cadherin gene in human gynecologic cancers.";

NAT. GENET. 7:98-102(1994).

-I- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTE

THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC

MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO

SORTING OF HETEROGENEOUS CELL TYPES. E-CADHERIN HAS A POTENT
                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BERX G., BECKER K.-F., HOEFLER H., "Mutations of the human E-cadherin HUM. MUTAT. 12:226-237(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BUSSEMAKERS M.J., GIROLDI L.A., VAN BOKHOVEN A., SCH
"Transcriptional regulation of the human E-cadherin
prostate cancer cell lines: characterization of the
gene promoter.";
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TRANSMEM
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                                                                                                                                                                                               PFAM;
PFAM;
                                                                                                                                                                                                                                                                             EMBL; Z13009; G31073; -.
EMBL; Z18923; G31075; -.
EMBL; X12790; G930046; -.
EMBL; L34545; G509605; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CANCER RES.
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MEDLINE; 98415721.
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                                                                                                                                                                                HSSP;
                                                                                                                                                                                                            MIM; 192090;
PROSITE; PS00232; CADHERIN;
PROCEDURE CADHERIN; 5.
                                                                                                                                                                                                                                    PIR; S25141; IJHUCE.
PIR; S37654; S37654.
MIM; 192090; -.
                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INVASIVE SUPPRESSOR ROLE.
SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: NON-NEURAL EPITHELIAL TISSUES.
DEFECTS OF CDH1 IS REGARDED AS ONE OF THE MAIN MOLECULAR
INVOLVED IN DYSFUNCTION OF THE CELL-CELL ADHESION SYSTEM,
TRIGGERING CANCER INVASION (GASTRIC, BREAST, OVARY, ENDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE CADHERIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND
                                                                                                                                                                    ADHESION; GLYCOPROTEIN;
                                                                                                                                                                                             PF00028; cadherin; 5.
PF01049; Cadherin_C_term;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THYROID) AND METASTASIS.
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                                                                                                                                                     REPEAT;
 27
154
882
707
731
731
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593
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                                                                                                                                                      SIGNAL;
                                         CYTOPLASMIC CADHERIN 1. CADHERIN 2.
 CADHERIN
CADHERIN
CADHERIN
                                                                                                                                                     PHOSPHORYLATION;
NAL; DISEASE MUTAI
                                                                                  POTENTIAL
                                                                                               EXTRACELLULAR (POTENTIAL)
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(CDH1) 9
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ENDOMETRIUM

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CADB_XENLA STANDARD; PRT; 9
733152;
01-OCT-1993 (REL. 27, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UP
15-JUL-1998 (REL. 36, LAST ANNOTATION
BLASTOMERE-CADHERIN PRECURSOR (B-CADHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                        MEDLINE; 9206581.

MEDLINE; 9206581.

MEDLINE; 9206581.

"Expression of XBCad, a novel cadherin, during oogenesis and early development of XBCad, a novel cadherin, during oogenesis and early development of XBCad, a novel cadherin, during oogenesis and early development of XBCad, in The STATE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

"I- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

"I- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES.

SORTING OF HETEROGENEOUS CELL TYPES.

"I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

"I- TISSUE SPECIFICITY: EXPRESSED IN PITUITARY GLAND, LUNG AND KIDNEY.

"I- DEVELOPMENTAL STAGE: DURING OOGENESIS AND EARLY DEVELOPMENT.

"SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
  EMBL; X78546; G468817; -. EMBL; X63719; G64567; -. PIR; S43065; S43065. TROSITE; PS00232; CADHERII
                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MECH. DEV. 47:213-22
[2]
SEQUENCE OF 459-905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MULLER H.A., KUHL M., FINNEMANN S
HAUSEN P., WEDLICH D.;
"Xenopus cadherins: the maternal
members of the family.";
                                                                                                                   or send an email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 95151580.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERE-CHUMANA, (INC.); LAEVIS (AFRICAN CLAWED FROG).
TA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA;
FRACHIA: PIPOIDEA; PIPIDAE; XENOPODINAE; XENOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                              requires a license agreement (:
an email to license@isb-sib.ch)
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53.8%;
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POTENTIAL.
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. 1.74e+00;
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IN LOBULAR BREAST CANCER).

IN LOBUSE GASTRIC CANCER).

IN DIFFUSE GASTRIC CANCER).

IN DIFFUSE GASTRIC CANCER).

IN DIFFUSE GASTRIC CANCER).

IN DIFFUSE GASTRIC CANCER).

IN THYROID CANCER).

IN DIFFUSE GASTRIC CANCER).

IN DIFFUSE GASTRIC CANCER).

IN DIFFUSE GASTRIC CANCER).
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N OVARIAN CANCER).
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CRC32;
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                                                                                                                                                                                                           restrictions
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AS SHAPIRO I., FANNON A.M., KWONG P.D., THOMPSON A., LEHMANN M.S.,

AS GRUEBEL G., LEGRAND J.-F., ALS-NIELSEN J., COLMAN D.R.,

AN HENDRICKSON W.A.;

AN HENDRICKSON W.A.;

AN "Structural basis of cell-cell adhesion by cadherins.";

ANATURE 374:327-337(1995).

C -!- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

C -!- FUNCTION: CADHERINS MAY THUS CONTRIBUTE TO THE

C MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE

C SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED IN

C NEURONAL RECOGNITION MECHANISM.

C -!- SUBCELLULAR. LOCATION: TYPE I MEMBRANE PROTEIN.

C -!- SUBCELLULAR. LOCATION: TYPE I MEMBRANE PROTEIN.
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Matches
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TAMURA K.
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLLINE; 89346748.
MIYATANI S., SHIMAMURA K., HATTA M.,
MATSUNAGA M., HATTA K., TAKEICHI M.;
"Neural cadherin: role in selective
SCIENCE 245:631-635(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
RODENTIA; SCIUROGNATHI; MURID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAD2_MOUSE
P15116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM;
PFAM;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NEURAL-CADHERIN PRECURSOR (N-CADHERIN).
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; PF01049; Cadherin_C_term;
; P09803; 1SUH.
ADHESION; GLYCOPROTEIN; PHO
     SWISS-PROT
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Similarity 50.0%;
7; Conservative
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ILT -> NSA (IN REF. 2).

R -> Q (IN REF. 2).

V -> A (IN REF. 2).

D -> N (IN REF. 2).

D -> N (IN REF. 2).

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ASP/GLU-RICH
POTENTIAL.
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EXTRACELLULAR (POTENTIAL).
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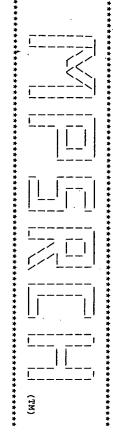
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CARBOHYD
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       SEQUENCE FROM N.A.
STRAIN-S288C / SEY6210;
MEDLINE; 97060018.
MEDLINE; 97060018.
*Identification of ASK10 as a multicopy activator of Skn7p-dependent transcription of a HIS3 reporter gene.";
YEAST 12:267-272(1996).
                                                                                  ASK10 PROTEIN
ASK10 OR YGRO97W.
SACCHAROMYCES CERRYISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBI outstation - the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as sits content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL ADHESION; GLYCOPROTEIN; PHOSPHORYLATION; CALCIUM-BINDING; REPEAT; SIGNAL; 3D-STRUCTURE.
YEAST
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; A32759; IJM;
; INGG; 10-JU;
; INCH; 10-JU
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CYTOPLASMIC (POTENTIAL).
CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
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                                                                                                                                                                                                                                                             Score 54; DB 1; I
Pred. No. 1.74e+00;
7; Mismatches 2
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                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
HERNANDEZ K., WEBER N., WIPFLI P., SCHMIDHEINI T.;
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
-I- FUNCTION: PUTARIVE ACTIVATOR OF SKN7.
-I- SIMILARITY: TO YEAST YILLOSC AND YNLO47C.
                                                                                                                                                                                           SGD;
                                                                                                                                   CONFLICT
                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                             DOMAIN
            692 TEKIVSPEPS 701
 6 AFKIVSQEPA 15
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Z72882; E243478;
                                                Similarity
                                                                            1146
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Pred. No. 1:
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1.74e+00;
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Search completed: Fri Jun 11 17:22:53 1999 Job time : 8 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:23:10 1999; MasPar time 6.15 Seconds 133.169 Million cell updates/sec

Tabular output not generated.

Scoring table: Sequence: Description: Perfect Score: Title: PAM 150 Gap 15 >US-08-991-628-3 (1-15) from US08991628.pep 96 LNSKIAFKIVSQEPA 15

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb19

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 25.449; Variance 30.607; scale 0.831

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

21121111111111111111111111111111111111	Result
	Score
\$	Query Match
1421 1421 1421 225 225 878 878 878 2258 878 2258 2258	Length
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03590 035907 P72670 P72670 Q20152 Q93345 Q93345 Q93345 Q93345 Q93345 Q93328 Q89328 Q89328 Q89328 Q893205 Q893205 Q893205 Q98705 Q28705 Q28706	IĐ
DESMOCLEIN 3 (FRAGMENT T19C21 7 PROTEIN. HYPOTHETICAL 16.6 KD P F38B7.4 PROTEIN. C36B1.11 PROTEIN. C36B1.11 PROTEIN. HYPOTHETICAL 12.3 KD P N-CADHERIN (FRAGMENT). UVOMORULIN PRECURSOR (LARGE PROTEIN. RNA POLYMERASE, SBT2. SERINE PROTEASE, SBT2. SERINE PROTEASE, SBT2. SERINE PROTEASE, FOTEIN Z RNA POLYMERASE PROTEIN RNA POLYMERASE PROTEIN. RNA POLYMERASE PROTEIN. RNA POLYMERASE PROTEIN. RNA POLYMERASE I. ORF248. E54D5.11 PROTEIN. N UTILIZATION SUBSTANC.	Description
3.46e-01 1.65e-01 2.10e+00 3.21e+00 3.21e+00 5.16e+00 5.16e+00 5.16e+00 6.24e+00 8.24e+00 8.24e+00 8.24e+00 8.24e+00 8.24e+00 8.24e+00 8.24e+00 8.24e+00 1.31e+01	Pred. No.

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3.23e+01 3.23e+01	3.23e+01	3.23e+01	3.23e+01	3.23e+01	3.23e+01	3.23e+01	3.23e+01	3.23e+01	2.06e+01	2.06e+01	2.06e+01	2.06e+01	2.06e+01	2.06e+01	2.06e+01	2.06e+01	1.31e+01	•	1.31e+01	1.31e+01	1.31e+01	1:31e+01	1.316+01

ALIGNMENTS

AC 035902; DT 01-JAN-1998 (TREMBLREL 05, CREATED) DT 01-JAN-1998 (TREMBLREL 05, LAST SEQUENCE UPDATE) DT 01-JAN-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE) DT 01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE) DE DESMOCILIUS (MOUSE). ON DSG3. SUSMISCULUS (MOUSE). OC SCIUROGNATH; MUTIDAE; MURINAE; MUS. RI (1) OC SCIUROGNATH; MUTIDAE; MURINAE; MUS. RI (1) RR SEQUENCE FROM N.A. RC STRAIN-BALB/C; RA ISHIKAWA H., LI K., UITTO J.; RR SEQUENCE FROM N.A. RC STRAIN-BALB/C; RA ISHIKAWA H., LI K., UITTO J.; RR PROSECLULLAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY) DE MEMBL; UB6016; G2290200; . PROSITE; PS0023; CADHERIN; 2. DR PROSITE; PS0023; CADHERIN; 2. PRAM: PF0028; CACHERIN; 4. RESULT 993 AA; 107888 MM; 881794BD CRC32; PFAM: PF00286; CACHERIN; 4. PFAM: PF00286; CACHERIN; 4. PFAM: PF00286; CACHERIN; 4. PFAM: PF00287; CACHERIN; 4. QUETY MATCH DR POSITE; PS0023; CACHERIN; 4. QUETY MATCH Best Local Similarity 93.3%; Pred. No. 3.46e-09; Matches 14; CONSERVATIVE 1; MISMATCHES 0; Indels 0; Gal DB 19 MNSKIAFKIVSQEPA 15 PROSITE; PS0028; CACHERIN; PROSITE; DS0027; PRELIMINARY; PRT; 1421 AA. COUCHY 1998 (TREMBLREL 08, CREATED) DT 01-NOV-1998 (TREMBLREL 08, LAST SEQUENCE UPDATE) DT 01-NOV-1998 (TREMBLREL 08, LAST SEQUENCE UPDATE) DT 01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE) DT 01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE) DT 01-NOV-1998 (TREMBLREL 08, CREATED) DT 01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE) DT 01-NOV-1998 (TREMBLREL 08, CREATED) DT 01-NOV-1998 (TREMBLREL O8, LAST ANNOTATION UPDATE) DE T19C21.7, PROTEIN. CC EUGHYLLOPHYTA; EMBRYOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA, EMBRYDDESIS SPERMATOPHYTA; MAGNOLLOPHYTA; EUDICOTYLEDONS; ROS:

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P72670; P72670;

Ol-Feb-1997 (TREMBLREL 02, CREATED)

Ol-Feb-1997 (TREMBLREL 02, LAST SEQUENCE U

Ol-ROV-1998 (TREMBLREL 08, LAST ANNOTATION

HYPOTHETICAL 16.6 KD PROTEIN.

SYNECHOCYSTIS SP. (STRAIN PCC 6803).

SYNECHOCYSTIS SP. (STRAIN FCC 6803).
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Q20152;
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Q1-NOV-1996 (TREMBLREL. (
Q1-NOV-1996 (TREMBLREL. (
Q1-JAN-1999 (TREMBLREL. (
E38B7.4 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.", DNA RES. 3:109-136(1996).
EMBL; D90899; D1017405; -.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRAND SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS SOMERVILLE C.R., VENTER J.C.;
"Arabidopsis thaliana chromosome II BAC T19C21 genomic SUBMITTED (AUG-1998) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL, ACO04683; G3395428; ...
SEQUENCE 1421 AA; 154325 MW; 1B6D2FF1 CRC32;
CAENORHABDITIS ELEGANS.
CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
SHARDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y., MIYAJIMA N., HIROSAWA M., SUGIURA T., SASAMOTO S., KIMURA T., HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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STRAIN-CV. COLUMBIA;
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Local Similarity 38.5%;
hes 5; Conservative
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larity 40.0%;
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Pred.
8; M
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Pred. No. 7.46e-01;
7; Mismatches 1
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d. No. 1.65e-01;
Mismatches 1;
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BANKS.
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                                                                        SEQUENCE FROM N.A.

XX MEDLINE; 94150718 ANDERSON K., BAYNES C., BERKS M.,

XX MEDLINE; 94150718 J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

XX MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

XX MILSON R., DURION J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

XX CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

XX GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

XX JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

XX LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

XX LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

XX LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

XX LIGHTNING J., FLOYD C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

XX PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

XX PARSONS J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

XX WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

TO CALL OF THE PROPERTY OF TH
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Q93345;
Q93345;
Q1-FEB-1997
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C36B1.11.
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EMBL; Z74033; E1346602; -.
SEQUENCE 225 AA; 26356 MW;
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EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
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                                                                      NATURE 368:32-38(1994).
EMBL; Z80215; E1344392; -
SEQUENCE 327 AA; 37139
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(TREMBLREL.)
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larity 80.0%;
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LAST ANNOTATION UPDATE
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1; 1
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                                                                        D8A2C259 CRC32;
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   Mismatches
                    55; DB 5; I
No. 3.21e+00;
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   Indels
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RESULT 6
ID 048607;
AC 048607;
AC 01-JUN-1998 (
DT 01-JUN-1998 (
DT 01-AUG-1998 (
DT 01-BUG-1998 (
DE HYPOTHETICAL
OS HORDEUM VUICAS
OC EUPHYLLOPHYTE
OC POACEAE; HORL
RN [1]
RP SEQUENCE FROM
RC STRAIN-ALBOST
RA HESS W.R., GC
RL SUBMITTED (DI
DR EMBL; AJ2227;
KW HYPOTHETICAL
FT NOW_TER
SQ SEQUENCE 1
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RESULT
AC Q1
DT 01
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Best Local S
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Q15855
Q15855; Q16194; Q13799;
01-NOV-1996 (TREMBLEEL 01
01-NOV-1996 (TREMBLEEL 01
01-NOV-1998 (TREMBLEEL 06
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O55075;
O1-JUN-1998 (TREMBLREL 06, C
O1-JUN-1998 (TREMBLREL 06, L
O1-AUG-1998 (TREMBLREL 07, L
N-CADHERIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRICETULUS GRISEUS (CHINESE HAMSTER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
SCIUROGNATHI; MURIDAE; CRICETINAE; CRICETULUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HESS W.R., GOLZ R., BOERNI
SUBMITTED (DEC-1997) TO EN
EMBL; AJ222776; E1203984;
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-ALBOSTRIANS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPUJIBLANDE - HYPUJIBLANDE (BARLEY).
HORDEUM VUIGARE (BARLEY).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYO
EUKARYOTA; VAGNOLIOPHYTA; MAGNOLIOPHYTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
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HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                               h 56.3%;
Similarity 40.0%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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238 AA;
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(TREMBLREL 06, LAST SEQUENCE UPDATE)
(TREMBLREL 07, LAST ANNOTATION UPDATE)
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larity 45.5%;
Conservative
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12250 MW;
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BOERNER T.;
) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                       26234 MW;
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                                                                                                                                                                                                                                                                                                         93
                                                    01, CREATED)
01, LAST SEQUENCE UPDATE)
08. LAST ANNOTATION UPDATE)
-CADHERIN) (ARC-1/UYOMORULIN).
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Pred. No. 5.
7; Mismatc
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Pred. No.
5; Misma
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LAST SEQUENCE LAST ANNOTED
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  VERTEBRATA;
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1. No. 5.16e+00;
Mismatches 2;
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ANNOTATION UPDATE)
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5.16e+00;
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MAMMALIA;
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LILIOPSIDA; POALES;
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                                                                                                                                                                                                                                                                                                                                                                                          Length 238;
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  EUTHERIA;
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                                                                                                                                                              guinea pigs.";
J. VET. MED. SCI
EMBL; AB012132;
                                                                                                                                                                                                                                                                                                                                                                                                                                     089238;
089238;
01-NOV-1998
01-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the cadherin superfamily BIOCHEM. BIOPHYS. RES. COMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 94306394.
BECKER K.F., ATKINSON M.J.,
SIEWERT J.R., HOFLER H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 333-472 FROM N.A.
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 94242050.
                                                                                                                                                                                                                                                                                   STRAIN-GP;
                                                                                                                                                                                                                                                                                                                                    LARGE PROTEIN
LARGE PROTEIN
LUMAN PARAINFLUENZA VIRUS 3.
VIRUSES; SSRNA NEGATIVE-STRAND VII
PARAMYXOVIRIDAE; PARAMYXOVIRINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRIXEN U.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CANCER RES.
                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                         OHSAWA K., YAMADA A., TAKEUCHI K., WATANABE Y., MIYATA H., "Genetic characterization of parainfluenza virus 3 derived
                                                                                                                                                                                                                                                                 MEDLINE;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00232;
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                                   866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 NAAIAYTILSQDP
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[TE; PS00232; CADHERIN; 3.
; PF00028; cadherin; 5.
; PF01049; Cadherin_C_term; 1.
; PF01049; Cadherin_C_term; TRANSMEMBRANE; ADHESION; GLYCOPROTEIN; POTENTIAL.
POTENTIAL.
                                 LDRSVLYRIMNOEPG 1012
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3 (TREMBLREL.
9 (TREMBLREL.
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2258 AA; 2588
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                                                                                                                                                                                    SCI. 60:919-922(1998).
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96741 MW;
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53.8%;
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                                                                                       56.3%;
33.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                   8,88
                                                                   Score 54;
Pred. No.
7; Misma
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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; 8F7F0180 CRC32;
                                                                                                                                                                                                                                                                                                                                            VIRUSES; MONONEGAVIRALES; 
AE; PARAMYXOVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200:1754-1761(1994)
                                                                         Mismatches
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No. 5.16e+00;
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                                                                 )B 1.,
,.16e+00;
3;
                                                                                                        DB 14;
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                                                                         Indels
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O43159;
O1-JUN-1998 (TREMBLREL. (
O1-JUN-1998 (TREMBLREL. (
O1-AUG-1998 (TREMBLREL. (
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DURBIN A.D.;

SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ

EMBL; U51116; G1262234; -.

PFAM; PF00946; Paramyx_RNA_Pol; 1.

SEQUENCE 2258 AA; 258927 MW; 4B7A664B
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081081;
081081;
01-NOV-1996
01-NOV-1998
                                                                                                                                                                                                                                               ISHIKAWA K., NAGASE T., NAKAJIMA D., SEKI N., TANAKA A., KOTANI H., NOMURA N., OHARA O.; SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA EMBL; AB007869; D1024586; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIAA0409,
HOMO SADIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIAA0409 (FRAGMENT).
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DURBIN A.D.;
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STOKES A., TIERNEY E.L., SARRIS C.M., MURPHY B.R., HALL The complete nucleotide sequence of two cold-adapted, temperature-sensitive attenuated mutant vaccine viruses cp...) derived from the JS strain of human parainfluenza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-JS;
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VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES; PARAMYXOVIRIDAE; PARAMYXOVIRINAE; PARAMYXOVIRUS.
                              416
                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-BRAIN;
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1 LNSKIAFKIVSQEPA 15
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les 5; Conser
TKLGFKIVSKD
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33.3%;
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Pred. No. 5.
7; Mismatc
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Pred. No. 8.24e-
4; Mismatches
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8.24e+00;
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                                                                                                                                                Length 464;
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01-MAY-1997 (TREMBLREL 0
01-JAN-1999 (TREMBLREL 0
01-JAN-1999 (TREMBLREL 0
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDA
SENDAI VIRUS (STRAIN Z) GENOME RNA 5'END (STRAIN
HUMAN PARAINFLUENZA 1 VIRUS
VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGA
PARAMYXOVIRIDAE; PARAMYXOVIRINAE; PARAMYXOVIRUS.
                                                                                                        SHIODA T., IWASAKI K., SHIBUTA H.;

"Determination of the complete nucleotide sequence of the Sendai virus genome RNA and the predicted amino acid sequences of the F, and L proteins.",

NUCLEIC ACIDS RES. 14:1545-1563(1986).

EMBL; X03614; G60900; -

FFAM; PF00946; PATAMYX_RNA_pol; 1.

SEQUENCE 1980 AA; 224006 MW; 4BAC22B0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Q84185
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                                                                                                                                                                                                                           SHIODA T.,
                                                                                                                                                                                                                                           MEDLINE; 86148492.
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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MENDEL; 8813; LYCes;1086;2.
PROTEASE; SERINE PROTEASE.
SEQUENCE 775 AA; 83115 M
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MEICHTRY J., AMRHEIN
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EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;

EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;

ESTERIDAE; SOLANANAE; SOLANALES; SOLANACEAE; SOLANUM.
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           725
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                                                             Local Similarity
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LDKQVLYRVMNQEPG
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46.78;
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26.7%;
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08, LAST ANNOTATION UPDATE)
GENOME RNA 5'END (STRAIN Z).
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Pred.
5; M
                                          Score 53; DB 14; LA Pred. No. 8.24e+00; 8; Mismatches 3;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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4BAC22B0 CRC32;
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8.24e+00;
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RESULT 14

ID 055528

DT 01-JUN-1998 (
DT 01-JUN-1998 (
DT 01-NOV-1998 (
DE RNA POLYMERAS
GN L.
OS SENDAI VIRUS.
OC VIRUSES; SERN
OC PARAMYXOVIRID
RN [1]
RP SEQUENCE FROM
RC STRAIN-ONITAL
RX MEDLINE; 9806
RX MEDLINE; 9806
RX ITOH M., ISSE
RI "ISOLATION fro
RT ISOLATION fro
RT LLC-MX2 Cells
RL J. GEN. VIROL
DR EMBL; AB000579
SQ SEQUENCE 22
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OC 055530;
DT 01-JUN-1
DT 01-JUN-1
DT 01-WN-1
DT 01-WN-1
DF RNA POLY
GN L.
OS SENDAI \
OC VIRUSES;
CC PARAMYX
(1)
RR SEQUENCI
RC STRAIN-(1)
RC STRAIN-(1)
RC STRAIN-(1)
RT MICLINE
RA HITOH M.
RT "ISOLAT.
RT mutation
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RL J. GEN.
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Best Local Similarity 26.7%;
Matches 4; Conservative
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Best Local Similarity 26.7%;
Matches 4; Conservative
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ITOH M., ISECAWA Y., HOTTA H., HOMMA M.;

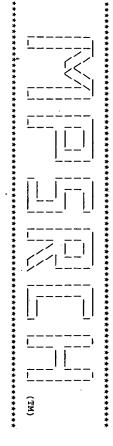
"Isolation of an avirulent mutant of Sendal virus with two amino acid mutations from a highly virulent field strain through adaptation to LLC-MK2 cells.";

J. GEN. VIROL. 78:3207-3215(1997).

EMBL; AB005795; D1025305; -.

SEQUENCE 2228 AA; 253058 MW; 8816E77F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SENDAI VIRUS.
VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES;
PARAMYXOVIRIDAE; PARAMYXOVIRINAE; PARAMYXOVIRUS.
                                                                                                                                                        ITOH M., ISBGAWA Y., HOTTA H., HOMMA M.;
"Isolation of an avirulent mutant of Sendal virus with two amino acid mutations from a highly virulent field strain through adaptation to LLC-MK2 cells.";
10. GEN. VIROL. 78:3207-3215(1997).
EMBL; ABOGS796; D1025314;
EMBL; ABOGS796; D1025314;
SEQUENCE 2228 AA; 253000 MW; A3058CCB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-VOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
RNA POLYMERASE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-VOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
RNA POLYMERASE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-OHITA;
                                                                                                                                                                                                                                                                                      WEDLINE; 98062143.
                                                                                                                                                                                                                                                                                                                                                                      VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES; PARAMYXOVIRIDAE; PARAMYXOVIRINAE; PARAMYXOVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       973 LDKQVLYRVMNQEPG 987
                                                                                                                                                                                                                                                                                                                                                                                                               SENDAI VIRUS.
                                      973 LDKQVLYRVMNQEPG 987
                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.
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      μ
LNSKIAFKIVSQEPA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                      253000 MW; A3058CCB CRC32;
                                                                             Score 53; DB 14; Length 2228; Pred. No. 8.24e+00; 8; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 53; DB 14;
Pred. No. 8.24e+00;
8; Mismatches 3
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                                                                           Gaps
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Search completed: Fri Jun 11 17:25:14 1999 Job time : 124 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Fri Jun 11 17:34:04 1999; MasPar time 4.88 Seconds 65.408 Million cell updates/sec

Title:

Description: Perfect Score: Sequence: 108 >US-08-991-628-4 (1-15) from US08991628.pep 1 TPMFLLSRNTGEVRT 15

Scoring table: PAM 150 Gap 15

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35 1:part1 2

34:part34 39:part39 i:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part14 15:part14 15:part14 15:part14 15:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 23:part28 29:part29 30:part20 31:part31 32:part37 33:part33 34:part34 35:part35 36:part26 37:part37 38:part38

Statistics: Mean 19.257; Variance 58.572; scale 0.329

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	₽ď	ID	Description	Pred. No.
<u>,</u>	108	100.0	15	ωį	W78815	Desmoglein 3 protein	6.54e-05
N	108	100.0	15	20	W04844		6.54e-05
ω	108	100.0	15	$\mathfrak{S}_{\mathfrak{S}}$	W64816		6.54e-05
4	108		614	19	W07908	Pemphigus vulgaris an	6.54e-05
տ	108		999	თ	R30742	Human pemphigus vulga	6.54e-05
0	88	81.5	778	21	W15489	Pemphigus foliaceus a	1.64e-02
7	61	56.5	583	Ŋ	R07999	Asparagine synthetase	1.82e+01
8	61	56.5	586	N	R07998	Asparagine synthetase	1.82e+01
9	00	55.6	163	34	W38654	S. pneumoniae asparta	2.33e+01
10	59	54.6	616	17	R86867	Rat protocadherin pc5	2.98e+01
11	57	52.8	. 263	24	W13010	Segment of desmosomal	4.84e+01
12	57	52.8	560	24	W13009	Segment of desmosomal	4.84e+01
13	55	50.9	660	13	R69633	Human interleukin-12	7.81e+01
14	55	50.9	662	3	R69632	Human interleukin-12	7.81e+01
15	55	50.9	662	21	W12772	Human interleukin-12	·7.81e+01
16	54	50.0	325	28	W33725	Mouse melanocortin-5	9.91e+01

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	1
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928 2								*									w	ω	w	w	w	w	-	w	N	_	ω	N
						4 P3								2 R2			80	α	æ	œ	œ	æ	9	σ	2 W	4 R	1 W	0
1017	5487	W19266	W40072	W03448	9929	930203	P30202	0023	0061	0877	0062	W38756	W70991	R24017	R10919	0206	5135	4156	W84155	5134	4154	5133	0365				7833	TOO
lori cytopla	rin		Human retinoid recept	Farnesoid-activated r	cylglucosam	γď	ed by	ein cor	nce of hu	Hook region #8 contg	Ĕ	osit	H	\sim	Humam GM-CSF receptor	Sequence encoded by p	yme	enz		A desaturase enzyme e	н	A desaturase enzyme e	Human cyclin B1.	տ	Ę.	Rat melanocortin rece	Mouse melanocortin-5	MORAGE METAMOCOT CTIT O
	in	2.52e+02	in	'n		2.52e+0	in	2.5	2.5	2.52e+0	2:			2.00e+01	.00e+0		.91e+0		9.91e+01			in	in	:~	in	in	.91e+0	. ATC.

ALIGNMENTS

expression product selected ironacids in length, having a seque fragment of a naturally-occurring protein a mammal; (2) a peptide having a mammal; (2) a peptide having bind to an MHC class I or I more peptide linked to a trafficking to W78897 are peptide fragments MPs are highly effective vehicle	PY gene therapy PS Disclosure; Page 8; 101pp; English. CC A microparticle preparation (MP) has been developed, consisting of CC A microparticles having a diameter of less than 100 mu m. The MP comprises: CC microparticles having a diameter of less than 100 mu m. The MP comprises: CC a) a polymeric matrix (PM) consisting of one or more synthetic polymers CC having a solubility in water of less that 1 mg/l; and (b) an expression CC vector selected from RNA molecules (at least 50% of which are closed CC circles) or circular plasmid DNA (at least 50% of which are supercolled). CC Also described is a MP of at most 20 microns in diameter, comprising: (a) CC also described is a MP of at most 20 microns in diameter, comprising: (b) CC Inked to a coding sequence, where the coding sequence encodes an	Synthetic. W09831398.A1. 23-JUL-1998. 22-JAN-1998; U01499. 26-JAN-1998; U5-003253. 22-JAN-1997; U5-787547. (PANG-) PANGAEA PHARM INC. CULLEY JM. Hedley ML, Langer RS, LI WPI; 98-427556/36. New preparations of microparticles matrix and nucleic acid comprising	RESULT 1 ID W78815 standard; peptide; 15 AA. AC W78815, DT 17-NOV-1998 (first entry) DE Desmoglein 3 protein fragment 206-220. KW Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen; KW class II associated peptide; pathogen; gene therapy; genetic disease; KW infection; downregulation; immune response. OS Homo sapiens.
n: (1) a polyperrue at reast / amand ance identical to the sequence of: (1) a na ng mammalian protein; or (11) a fragment of from an infectious agent which infects a length and sequence which permits it to lecule; and (3) the polypeptide or the sequence. W69763 to W69765, and W78793 for use in the present invention. The essent the delivery of polynucleotides	developed, consisting of than 100 mu m. The MP comprises: one or more synthetic polymers 1 mg/1; and (b) an expression ast 50% of which are closed 50% of which are supercoiled). In a find the sequence operatively lon control sequence operatively sequence encodes an appropriate of the sequence of the sequence operatively sequence encodes an appropriate operation of the sequence operatively sequence encodes an appropriate operation of the sequence operative operation of the sequence operation operation of the sequence operation of the sequence operation	unsford LB; - comprising a synthetic polymer an expression vector for use in	; autoantigen; tumour antigen; se therapy; genetic disease;

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RESULT ID WHAT ARC WE DIT 2 DE DE DE DE DE DE NEW AND PN OS HH PD 2 PF 2
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                                                                                                                                                                                                                                                                                                                                                      ratio-immune disease

Claim 1; Page 40; 58pp; English.

Chaim 1; Page 40; 58pp; English.

Ceither an isolated human non-collagen or non-myslin basic protein

(MBP) polypeptide which is capable of tolerising an individual to an

autoantigen; or an isolated human pathogen polypeptide capable of

tolerising an individual to that polypeptide. In both cases, the

polypeptide (whether self or non-self) includes an amino acid

sequence corresponding to a sequence motif for a MHC class II

sequence corresponding to a sequence with a human autoimmune

clisease and which binds to the polypeptide to activate autoreactive

Totelis, such as HIA-DR, which is associated with a human autoimmune

darived from the human desmoglein a protein (amino acids 206-220)

and is implicated as a self epitope in pemphigus vulgaris. Peptides

common 15 an.
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Best Local S
Matches 1
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Self epitope of desmoglein 3, implicated in autoimmune disease.
Tolerisation; self-epitope; antigen; autoimmune disease;
autoantigen; HLA; human leukocyte antigen; T-cell; thymocyte;
pemphigus vulgaris; desmoglein; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W04844 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    into phagocytic cells. The treating genetic diseases, an immune response.
                             Homo sapiens.
US5783567-A.
                                                     29-SEP-1998 (first entry)
Desmoglein-3 206-220.
Desmoglein; DG; gene therapy; pemphigus vulgaris; autoantigen; autoimmune disease; MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens - useful in disease treatment, and method for identification of other self and non-self antigens implicated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 96-425218/42.
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07-MAR-1996; U03182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
WO9627387-A1.
                                                                                                                                W64816 standard; peptide; W64816;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nerpes simplex virus; adenovirus; phosphomannomutase; numan papillomavirus; Epstein-Barr virus; DNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ınfluenza; haemagglutinin; reovirus; sigma protein.
                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                Match
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Similarity 100.0%;
15; Conservative
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Similarity 100.0%;
15; Conservative
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                                                                                                                                                                                                                                                                             Score 108; DB 20;
Pred. No. 6.54e-05;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 108; DB 35;
Pred. No. 6.54e-05;
0; Mismatches 0;
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PS Disclosure; Column 4; 42pp; English.

CC The patent describes a new preparation of microparticles each

CC comprising a polymeric matrix and a nucleic acid. The polymeric

cc matrix consists of one or more synthetic polymers having a solubility

CC in water of less than 1 mg/l (e.g. poly-lactic-co-glycolic acid);

CC and at least 90% of the microparticles have a diameter of less than

CC 100 microns. The microparticles are useful for the delivery of nucleic

CC acids to phagocytic cells. In one embodiment the microparticles are

CC less than 20 microns in diameter and the nucleic acid (preferably in

CC closed circular form) includes an expression control sequence

CC of the coding sequence is a polypeptide having a length and a sequence

CC which permits it to bind to an MHC class I or II molecule. The

CC expression product is thus an effective stimulator of an immune

CC response in mammals. The present sequence, an antigenic portion of

CC desmoglain 3, is an example of an MHC class II peptide which can be

CC expressed by the nucleic acid. It is associated with pemphigus

CC converse.
                                                                                                                   Query Match
Best Local S
Matches 1
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Matches 1
                                                                                                                                                                                                                                          pemphigus
Sequence
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                                                                                                                                                                                                                                                                                            Fused protein recognised by pemphigus vulgaris auto:antibody useful to treat and diagnose pemphis vulgaris claim 1; Page 7-9; 9pp; Japanese.
W07908 represents the human pemphigus vulgaris (PV) antigen extracellular region. The PV antigen is produced in patients with pemphis vulgaris resulting in autoimmune disease. PV is a rare relapsing disease causing suprabasal, intra-epidermal bullae (vesicles) of the skin and mucuous membranes, which is fatal if untreated. The PV antigen was fused to a human IgCl hinge region and the resulting fusion protein is useful to treat or diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pemphigus vulgaris antigen protein extracellular region. Autoantibody; immunoglobulin G; IgGl; fusion protein; ditreatment; pemphigus vulgaris; PV; bulla; blister; skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microparticle encapsulated nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-1995; 165632.
30-JUN-1994; JP-173291.
(NISH/) NISHUKAWA T.
WPI; 96-388562/39.
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                                                           205
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Local Similarity 100.08;
Nes 15; Conservation
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                                  tpmfllsrntgevrt 219
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                                                                                                                                                   Similarity
                                                                                                                                                                                                                                          vulgaris.
614 AA;
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larity 100.0%;
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. No. 6.54e-05;
Mismatches 0;
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No. 6.54e-05;
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                                                                                                                                                                               Length 614;
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SOCCCOST PRINTERS OF THE PRINT
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197798918-A.
US7798918-A.
15-DEC-1992: 798918.
27-NOV-1991: US-798918.
PR 27-NOV-1991: US-798918.
(USSH) US DEPT HEALTH & HUMAN SERVICE.
"" (USSH) US DEPT HEALTH & HUMAN SERVICE.
"" M, Klaus-Kovtun V, Stanley JR;
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                                                                                                                     remphigus foliaceus antigen-IgG constant region fusion protein - linked through the hinge region used to treat pemphigus foliaceus Claim 1; Page 10-12; 17pp; Japanese.

This sequence represents a fused protein recognised by pemphigus foliaceus the constant region of pemphigus foliaceus is a chronic, generalised, vesicular and scaling skin eruption similar to dermatitis herpetiformis. The pemphigus foliaceus is a chronic, generalised, vesicular and scaling skin eruption similar to dermatitis herpetiformis. The pemphigus foliaceus antigen fusion protein is useful to treat pemphigus foliaceus. The antigen is especially administered through an adsorbent upon which the fusion useful for detecting pemphigus foliaceus antibodies which is useful in immunocalignosis. The fusion protein has little or no side effects.
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Best Local S
Matches 1
  Best Local
Matches
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12-SEP-1995;
12-SEP-1995;
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Pemphigus foliaceus antigen-IgG constant region fusion protein.
Pemphigus foliaceus; autoantibody; constant region; IgG;
extracellular region; antigen; hinge portion; skin;
dermatitis herpetiformis; fusion protein; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is the pemphigus vulgaris 130kD antigen. The protein and its encoding DNA may be used in the diagnosis and treatment of pemphigus vulgaris. It is thought that the antigen may be a cell adhesion molecule.

Sequence 999 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding pemphigus vulgaris a diagnostic and therapeutic uses Disclosure; Fig 7; 50pp; English.
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Pemphigus vulgaris; skin disease; autoantibodies;
keratinocyte cell surface antigen; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W15489 standard; W15489;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; T66428.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NISH/) NISHIKAWA T.
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                                                                                                       immunodiagnosis.
quence 778 AA;
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  Similarity 66.7%
10; Conservative
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larity 100.0%;
Conservative
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                           81.5%;
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Pred. No. 6.54e-05;
0; Mismatches 0
  Score
Pred.
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e 88; DB 21; L
. No. 1.64e-02;
Mismatches 0;
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                                                 Length 778;
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15-NOV:1990,
02-MAY-1990, U02443.
03-MAY-1989, US-347302.
26-APR-1990, US-514816.
(UYRO-) ROCKFELLER UNIV.
                                                                                                                                          R0/990;
26-FBB-1991 (first entry)
Asparagine synthetase AS1.
asparagine synthetase; transgenic plant; herbicide resistance;
asparagine synthetase; nitrogen fixation; pea:
                                                                                                                                                                                                                                                                                                                                                                                                                            transgenic plants
Disclosure; Fig 2B; 9lpp; English.
Disclosure; Fig 2B; 9lpp; English.
The DNA sequence encoding this protein was isolated from cDNA clones selected from a pea nodule cDNA library from the "Sparkle" variety of P.sativum. Pea ASI CDNA was used as a probe.
The protein is produced by expression vectors containing the AS2 coding sequence. Recombinant AS can be used to engineer herbicide resistance, as a dominant selectable marker, to select novel
                                                                                                                                                                                                                                                                                                                                          A comparison of pea AS and human AS polypeptides reveals homology of 47% at the amino acid level, c.f. 86% between AS2. There are several regions of high local homology (g. 80%) shared between the pea AS and human AS polypeptides see also Q06598, Q06622 and Q06623.

Sequence 583 AA;
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26-FEB-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          culture, etc.
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WPI; 90-361471/48.
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R07998;
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/label= 8
486..500
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2; N
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homology
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% between AS1 and
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TRESULT PROPERTY OF THE SULT P
Claim 12; Page 407; 483pp; English.

Chis sequence represents a Streptococcus pneumoniae protein that, based to nomology with an Escherichia coli protein, is a aspartate ammonia con industrial sequence of the invention.

Classe, and is encoded by a DNA sequence of the invention.

Classe, and is encoded by a DNA sequence of the invention of the invention can be used to identify compounds which interact with and continuous pneumoniae proteins. Antagonists can be used to identify compounds which interact with and continuous to a tivate the activity of the proteins. Antagonists can be used to treat diseases caused by S. pneumoniae proteins, through genetic confinibit or activate the activity of the proteins. Antagonists can be considered to induce an immunological response confinition in they can also be used to induce an immunological response coffine encoding nucleic acids in a vector adequate to produce antibody cand/or T cell immune responses to protect the animal from disease. The proteins can also be used to identify antimicrobial compounds which are capable of inhibiting their bloactivity. In particular the proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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26-APR-1990; US-514816.
(UYRO-) ROCKFELLER UNIV.
COTUZZI GM, TSA1 FY;
WPI; 90-361471//0
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Disclosure; Fig 2A; 91pp; English.
The DNA sequence encoding this protein was isolated from cDNA clones selected from a pea nodule cDNA library from the "Sparkle" variety of P. sativum. Human AS cDNA was used as a probe.
The protein is produced by expression vectors containing the AS1 coding sequence. Recombinant AS can be used to engineer herbicide resistance, as a dominant selectable marker, to select novel
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15-NOV-1990.
02-MAY-1990;
03-MAY-1989;
26-APR-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W38654
W38654;
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See also 006599,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel Streptococcus pneumoniae proteins and related DNA - u diagnosing anti-microbial agents for treatment of bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; T98699.
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14-MAY-1997; U07950.
14-MAY-1996; US-017670.
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Similarity 77.8%;
7; Conservative
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/label= putative glutamine binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q06622 and Q06623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EECHAM CORP.
EECHAM PLC.
, Knowles DJC,
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Pred. No. 1.82e+01
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nicholas RO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synchronising plant cells in
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RESOLT ID WILL ACC WI

Segment of desmosomal cadherin, desmoglein Dsg2.
Desmosomal cadherin; desmoglein; Dsg2; cell; surface;
carcinoma; desmosome; antibody; epitope; diagnosis; de
micrometastasis; separation; enrichment; targetted del

micrometastasis; metastatic.

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1 TPMFLLSRNTGEV

W13010

standard;

protein;

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W13010;

21-NOV-1997 (first entry)

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                    밁
                                                                                                                                             Prolynucleotide(s) encoding human protocadherins pc3 and pc4 and rat profit involved in cell-cell adhesion and regulation activities pc5 - involved in cell-cell adhesion and regulation activities pc5 - fivolved in cell-cell adhesion and regulation activities pc5 - fivolved in cell-cell sc1 adhesion and postess for three protocadherins. This cc R8685-R86867 represent the sequences for three protocadherins are crelated to cadherin, and possess cell adhesive ability. Cadherins are composed of an N-terminal extracellular domain cathesion. Cadherins are composed of an N-terminal extracellular domain continuous continuous continuous and continuous and continuous continuous catherins and other cytoplasmic domain interacts with the cytoplasmic domain. The cytoplasmic domain interacts with the cytoplasmic domain is not present in all cadherins, but in those which possess it, it is essential for the cadherins, but in those which possess it, it is essential for the cadherins adhesive function. The cadherins which do not possess a cytoplasmic domain appear to function via a different method from those with a cytoplasmic domain. The continuous well and 2 (see T03575 and continuous c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
                                                                Matches
                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DOHE-) DOHENY EYE I
Suzuki S;
WPI; 96-068873/07.
N-PSDB; T03574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the invention can be used to prevent adhesion of bacteria to mammalian extracellular matrix proteins on in-dwelling devices or in wounds, to block protein-mediated mammalian cell invasion, and to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or other surgical techniques. Sequence 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 10
R86867;
R86867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9600289-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           catenin; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUN-1995; U08071.
27-JUN-1994; US-268161.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protocadherin; pc3; pc4; pc5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-AUG-1996
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85 tplfqlnentgei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 60.0% nes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                Conservative
                                                                                   54.6%;
                    97
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Pred.
3; M
                                                                                Score 59; DB 17;
Pred. No. 2.98e+01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; rat; cadherin; cell adhesion;
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                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.
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2.33e+01;
-hes 2;
                                                                2
                                                                                                        Length 616
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160 pvfylnkdtge1

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CC The present sequence is a segment of the desmosomal cadherin (DC), CC desmoglein Dsg2, which is exposed on the surface of epithelial or CC arcinoma cells and not bound to desmosomes. An antibody (Ab) CC directed against epitopes of the present sequence can be used to CC diagnose, i.e. to detect carcinoma cells, especially micrometastases, not bound to desmosomes. An antibody and CC as a therapeutic to deliver agents, e.g. other Ab or toxins, to CC target cells. The Ab provides rapid and reliable detection of CC metastatic carcinoma, and detects parts of DC that are not accessible in desmosome bound cells, as in normal tissue or
                                                                                                                                                                                                     Antibody reactive with part of desmosomal cadherin - exposed on surface of epithelial or carcinoma cells, not bound to desmosomes, yeseful for diagnosis and treatment of carcinoma micrometastases of claim 7; Page 5; 8pp; German.

The present sequence is a segment of the desmosomal cadherin (DC), desmoglein Dsg2, which is exposed on the surface of epithelial or carcinoma cells and not bound to desmosomes. An antibody (Ab) directed against epitopes of the present sequence can be used to directed against epitopes of the present sequence can be used to diagnose, i.e. to detect carcinoma cells, especially micrometastases, not bound to desmosomes to separate, enrich or detect living or fixed carcinoma cells by cell sorting methods and as a therapeutic to deliver agents, e.g. other Ab or toxins, to metastatic carcinoma, and detects parts of DC that are not accessible in desmosome bound cells, as in normal tissue or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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          Matches
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23-AUG-1995; DE-031033.
(PROG-) PROGEN BIOTECHNIK GMBH.
Franke WW, Schaeter S;
WPI; 97-146518/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Segment of desmosomal cadherin, desmoglein Dsg2.
Desmosomal cadherin; desmoglein; Dsg2; cell; surface; epithe carcinoma; desmosome; antibody; epitope; diagnosis; detectio micrometastasis; separation; enrichment; targetted delivery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-AUG-1995; DE-031033.
(PROG-) PROGEN BIOTECHNIK GMBH.
Franke WM, Schaefer S;
WPI; 97-146518/14.
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27-FEB-1997.
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23-AUG-1995; 031033
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6; Conser
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                                                                                                                                                 560
   52.8%;
larity 50.0%;
Conservative
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larity 50.0%;
Conservative
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Pred. No. 4.84e+01;
   Score 57; DB 20
Pred. No. 4.84e-
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                    DB 24; I
4.84e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ell; surface; epithelial;
diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 263
                                                                     Length 560
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       Indels
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R69633
R69633;
                                                                              DNA encoding a low affinity interleukin-12 receptor - used to bind or scavenge IL-12 to cause immune suppression, e.g. to suppress graft-vs-host reaction, and user impression or inflammation, and to treat autoimmune conditions claim 4; Page 31-33; 61pp; English.

A cDNA library of PHA-activated peripheral blood mononuclear cells in vector PEF-BOS was screened for interleukin-12 (IL-12) receptor cDNAs by panning. One isolated cDNA (083844) encoded a 662-amino acid low affinity IL-12 receptor (R69632). Another cDNA contained an additional 202 bp of 3'UTR; the deduced 660-amino acid sequence contained an additional sequence and the sequence of the s
                                                                                                                                                                                                                                                                                                           (HOFF ) HOFFMANN LA ROCHE Chizzonite RA, Chua AO, WPI; 95-076349/11.
                                                                                                                                                                                                                                                                                                                                                                            08-JUL-1994; 110657.
19-JUL-1993; US-094649.
19-JUL-1993; US-094713.
31-MAY-1994; US-248532.
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15-FEB-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunosuppressive;
inflammation; auto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interleukin-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human interleukin-12 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-SEP-1995
                (R69633) showed an altered C-terminal sequence compared to Recombinant IL-12 receptor was expressed in COS cells, and used for therapeutic or diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
therapeutic
660 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor; IL-12; immur
ive; graft-versus-host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "conserved 618..629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "sequence motif of cytokine receptor
superfamily Cys52..Cys62Sw"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456..458
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(W222SKWS)"
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'note- "conserved area of cytopiasmic tail"
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'note- "conserved area of cytoplasmic tail"
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Gubler UA,
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                                                                                                                                                                                                                                                                                                                                     Truitt
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Query Match Best Local

Similarity

53

. 99;

Score 55; Pred. No.

DB 13; 7.81e+01;

Length 660;

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Query Match
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19-JUL-1993; US-094649.
19-JUL-1993; US-094713.
31-MAY-1994; US-248532.
(HOFF ) HOFFMANN LA ROCHE & Chizzonite RA, Chua AO, G
                                   DNA encoding a low affinity interleukin-12 receptor - used to bind or scavenge IL-12 to cause immune suppression, e.g. to suppress graft-vs-host reaction, allograft rejection or inflammation, and to treat autoimmune conditions Claim 4; Page 24-27; Slpp; English.

A cDNA library of PHA-activated peripheral blood mononuclear cells in vector pEF-BOS was screened for interleukin-12 (IL-12) receptor cDNAs by panning. An isolated cDNA was sequenced (Q83844); it encoded a 662-amino acid low affinity IL-12 receptor (R69632). Recombinant IL-12 receptor was expressed in COS cells, and can be used for therapeutic or diagnostic purposes.
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52..64
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superfamily Cys52..Cys62Sw"
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       New interleukin-12 beta-2 receptor and high binding affinity complexes - have a high affinity for interleukin-12, and are used to recomplexes - have a high affinity for interleukin-12, and are used to recomplexes - have a high affinity for interleukin-12 (IL-12) receptor beta-1 receptor (W12772) and a low binding affinity for IL-12, but when complexed with an interleukin-12 (IL-12) receptor beta-1 receptor was a complex with a low binding affinity for IL-12. Its amino acid sequence was deduced from a cDNA clone (T59732) obtd. from human lymphoblasts. IL-12 receptor beta-1 can be expressed on the surface of transformed host cells as a complex with co-expressed IL-12 receptor beta-2, and used in therapeutic compsns. pref. with at least 1 cytokine antagonist, to treat autoimmune dysfunctions such as rheumatoid arthritis, inflammatory bowel disease and multiple sclerosis. The receptor protein or complex can also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity Matches 7; Conser
                                                                                                                                                                                                                                                  (HOFF ) HOFFMANN LA ROCHE Gubler UA, Presky DH; WPI; 97-147515/14.
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Interleukin-12 beta-1 receptor; IL-12; autoimmune rheumatoid arthritis; inflammatory bowel disease;
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                                                                                                                                                                                                                                    N-PSDB; T59732
                                                                                                                                                                                                                                                                                            26-FEB-1997.
23-JUL-1996; 111807.
01-AUG-1995; US-001701
30-MAY-1996; US-018674
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Conservative
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456..458
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(Cys52..Cys62SW)
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/note= "signal peptide cleavage site alternatively
follows Ala-23 ir Cys-24"
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'note= "cytokine receptor superfamily motif
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/note= "cytokine receptor superfamily motif
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Jok	Qy Db	7 m 0	SQ
Search completed: Fri Jun 11 17:35:53 1999 Job time : 109 secs.	14 Iflisrggaacrt 26 : : 3 MELLSRNTGEVRT 15	Query Match 50.9%; Score 55; DB 21; Length 662; Best Local Similarity 53.8%; Pred. No. 7.81e+01; Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;	Sequence 662 AA;

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c).1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:32:12 1999; MasPar time 4.36 Seconds 137.938 Million cell updates/sec

Tabular output not generated.

Title: >US-08-991-628-4
Perfect Score: 108
Sequence: 1 TPMFLLSRNTGEVRT 15

scoring table: PAM 150 Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir60

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 27.020; Variance 36.303; scale 0.744

SUMMARIES

22222111111111111111111111111111111111	Result No.
108 888 888 861 861 861 861 861 87 87 87	Score
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IJHUG3 IJHUG1 IJHUG1 S55982 S55694 S55682 AJPMN2 S50482 AJPMN2 S60482 AJPMN1 T03602 AJPCN IJ6645 JH071 A56450 A56400 S38673 D71089	Ħ
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Query Match 100.0%; Best Local Similarity 100.0%; Matches 15; Conservative

Score 108; DB 1; Length 999; Pred. No. 2.99e-11; 0; Mismatches 0; Indels 0;

Gaps

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45	44	43	42	41	40	39	38	37	36	35	34	သ	32	31	30	29	28	27	26	25	24
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dual specificity phos	probable ATP-dependen	hypothetical protein	cyclin Bl - human	cyclin B - rat	omega-3 fatty acid de	melanocortin-5 recept	melanocortin receptor	regulatory protein fn	transcription activat	gene B protein - alce	hypothetical protein	E6 protein - human pa	T-cell receptor beta	polynucleotide adenyl	IL12 receptor compone	citrate (si)-synthase	hypothetical protein	probable corA protein	H+-transporting ATP s	hypothetical protein	asparagine synthase (
3.17e+01	2.12e+01	2.12e+01	2.12e+01	2.12e+01	2.12e+01	2.12e+01	2.12e+01	2.12e+01	2.12e+01	2.12e+01	2.12e+01	2.12e+01	2.12e+01	1.41e+01	1.41e+01	1.41e+01	1.41e+01	1.41e+01	1.41e+01	1.41e+01	9.34e+00

ALIGNMENTS

Out of the ball	SUMMARY	937-966 110,180,545	910-938	610-639	496-598	390-495	270-383	160-267	52-157	\$0-615	50-999	24-49	1-23	FEATURE	10100	KEYWORDS	CLASSITTOATION	CTOT++DOOT CEM#	*50.00	GENETICS:	##01088-16	### HO (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	######################################	###O TO TO TO	#20003100	#CTORG-TOFOTO	#title	#journal	#authors	REFERENCE	ACCESSIONS	DATE	ORGANISM	TITLE	ENTRY	מפתות ח
	predicted #length 999 #molecular-weight 107502 #checksum 8311	desmoglein repeat #label g_site carbohydrate (Asn)		transmembrane	cadherin repeat homology #label CR5\	cadherin repeat homology #label	homology #label	cadherin repeat homology #label	cadherin repeat homology #label CR1\	#AOMA'n pytragodiniar #status predicted #label EXTV	<pre>#product desmoglein homolog #status predicted #label</pre>	<pre>#domain propeptide #status predicted #label PRO\</pre>	#domain signal sequence #status predicted #label SIG\	F			#supperfamily cadherin: cadherin repeat homology		\$500 CTU. 134030 CYTY. 150515	C75.7502	STETEMOROUS OD:WIGHOUP NID: \$150/01/ FIX: \$150/014	ference CB.W76/83: NTD.G100751:	##TDQ1/4100	TYPE MRNA	A41088	pemphigus vulgaris, a disease of cell adnesion. #croes-references MITD-92069753	a novel epi	67:869-877	Amagai, M.; Klaus-Kovtun, V.; Stanley, J.R.	A41088	10-Sep-1996 A41088	30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change	#formal_name Homo sapiens #common_name man	desmoglein 3 precursor - human	IJHUG3 #tvpe complete	

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Poynter, D.; Arnemann, J.; Rutman, A.J.; Pidsley, S.C.;
Watt, F.M.; Rees, D.A.; Buxton, R.S.; Magee, A.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:4796-4800
Desmosomal glycoprotein DGI, a component of intercellular desmosome junctions, is related to the cadherin family occli adhesion molecules.

#cross-references MUID:91271279
#accession A39706
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50-548
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Rees, D.A.; King, I.A.; Magee, A.I.

#journal Biochem. Soc. Trans. (1991) 19:1060-1064

#title Desmosomal glycoproteins I, II and III: novel members of the

cadherin superfamily.

#cross-references MUID:92175187
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PNCE A39706
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ip_position 18q12.1-18q12.2
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firication #superfamily cadherin; cadherin repeat homology
calcium binding; cell adhesion; duplication; glycoprotein;
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J. Cell Sci. (1991) 99:809-821
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                                                                                                                                                                                                                                                                                                       #title Desmoglein shows extensive homology to the cadherin cell adhesion molecules.
#cross-references MUID:91097553
#accession A37785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #journal Eur. J. Cell Biol. (1991) 55:200-208
#title Complete amino acid sequence of the epidermal desmoglein
precursor polypeptide and identification of a second ty
of desmoglein gene.
#cross-references_MID:92037656
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##cross references GB:M58165; NID:g162966;
NICE S38721
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Similarity 66.7%;
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Complete sequence of the desmoglein precursor and evidence for the existence of different desmoglein genes expressed in cell type-specific patterns.
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                              Koch, P.J.; Walsh, M.J.; Schmelz, Eur. Cell Biol. (1990) 53:1-12 Identification of desmoglein, a co
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##residues 44-1001,'AQPPSAT' ##label KO3
##cross-references GB:X57784
##note this sequence has been revised in
$38721
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                                                                                                                                                                                                       ##residues 1-572 ##label VAN ##cross-references EMBL:X83099; NID:g642340; PID:g642347
                     ##cross-references EMBL: Z72909;
MIPS: YGR124w
                                                         ##molecule_type DNA
##residues 1-572 ##label VAW
##experimental_source
                                                                                                                                                                                                                                                 ##molecule_type DNA
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                                                                                                                                                                                                                                                                                           van Dyck, L.; Goffeau, A. submitted to the EMBL Data Library, December 1994 Genes for an asn synthase, a GLFG-motif nucleoporin and a putative homeobox-domain protein are identified on a 18.3 kb segment of the yeast chromosome VII also carrying MEP1, ppT1, tree new ORFs, remnants of Ty and three tRNA genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yeast (Saccharomyces cerevisiae)
protein G6356; protein YGR124w
#formal_name Saccharomyces cerevisiae
23-aug-1995 #sequence_revision 19-Oct+1995
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calcium binding; cell adhesion;
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llarity 60.0%;
Conservative
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Talla, E.;
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asparagine synthase (glutamine-hydrolyzing)
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#domain cadherin repeat homology #label CR4\
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                                                                                                                        L.; Skala, J.; de Wergifosse, P.; Purnelle, E.; Nawrocki, A.; Del Bino, S.; Goffeau, A. to the Protein Sequence Database, May 1996
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Pred. No. 7.
5; Mismatc
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duplication; glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##residues 1-572 ##label FUL
##cross-references EMBL:U40829; NID:gl066476; PID:gl066479; MIPS:YPR145w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type DNA
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##cross-references EMBL:248675; NID:gl163061; PID:g747902
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- yeast (Saccharomyces cerevisiae)
protein P659.3; protein YRR145w
#formal_name Saccharomyces cerevisiae
19-May-1995 #sequence_revision 01-Sep-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, March 1995 Multiple regulatory systems control expression of the Saccharomyces cerevisiae ASN1 and ASN2 genes at the
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                                  hypothetical protein 6 precursor - Salmonella #formal_name Salmonella typhimurium 19-Mar-1997 #sequence_revision 25-Apr-1997 #te 17-Mar-1999
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#length 572 #molecular-weight 64470 #checksu
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#journal Mol. Microbiol. (1993) 8:543-558

#title Nuclectide sequence of a 13.9kb segment of the 90kb virulence plasmid of Salmonella typhimurium: the presence of fimbrial *cross-references MUID:93316852

#accession S32892
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#title
                                                                                                                                                             #authors Crooke, H.; Cole, J.
#authors Crooke, H.; Cole, J.
#journal Mol. Microbiol. (1995) 15:1139-1150
#title The biogenesis of c-type cytochromes
requires a membrane-bound protein,
disulphide isomerase-like domain.
#cross-references MUID:95349398
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##cross, references EMBL:L08613
# #length 295 #molecular-weight 31162 #checksum
                 ##residues 'M', 78-565 ##label RE2
##cross-references EMBL:X77707; NID:9871027; PID:9871029
##note in this report, the codon GTG for Val-77
##anote as a start codon
                                                                                                                                                                                                                                                                                                              ##cross-references EMBL: 236905; NID:g535290; PID:g581055
##note in this report, the codon GTG for Val-77 was interpreted
as a start codon
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##residues 'M',78-565 ##label RES
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##note the nucleotide sequence was submitted to
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##residues 1-565 ##label BUR
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Local Similarity 80.0%;
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Mol. Microbiol. (1995) 15:1127-1137
Molecular genetics of a chromosomal locus involved
tolerance in Escherichia coli K-12.
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Nucleic Acids Res. (1995) 23:2105-2119
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#cross-references MUID:97426617
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                                                                                                                                   ##cross-references EMBL:U18778;
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#length 923 #molecular-weight 103333
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hypothetical protein YER024w - yeast (Sacc)
cerevisiae)
#formal_name Saccharomyces cerevisiae
28.May-1993 #sequence_revision 24-Feb-1995
21-Nov-1997
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submitted to the EMBL Data Library, February 1994
The biogenesis of C-type cytochromes in Escherichia coli
requires an integral membrane protein with a protein
disulphide isomerase like domain.
                                                                                                                                                                                                           submitted to the EMBL Data Library, December 1994 The sequence of S. cerevisiae cosmids 9537, 9581, and lambda clone 5898.
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inner membrane; redox-active disulfide; transmembrane
#length 565 #molecular-weight 61795 #checksum 2685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shav
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   Score 63; DB 2; 1
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4; Mismatches
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                 Match 56.5%; Local Similarity 77.8%;
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Similarity 77.8%;
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EMBO J. (1990) 9:323-332
Dark-induced and organ-specific expression of two asparagine synthetase genes in Pisum sativum.
                                                                                                                                                                                                                                                                       Waterhouse, R.N.; Smyth, A.J.; Massonneau, A.; Prosser, I. Clarkson, D.T.
Plant Mol. Biol. (1996) 30:883-897
Molecular cloning and characterisation of asparagine synthetase from Lotus Japonicus: dynamics of asparagine synthesis in N-sufficient conditions.
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asparagine biosynthesis; ligase
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                                                                 #superfamily asparagine synthase (glutamine-hydrolyzing)
asparagine biosynthesis; ligase
#length 586 #molecular-weight 66461 #checksum 3372
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asparagine synthase (glutamine-hydrolyzing)
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31-pec-1991 #sequence_revision 31-Dec-1991 #text_change
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th 583 #molecular-weight 65649 #checksum 2836
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#journal EMBO J. (1990) 9:323-332
#title Dark-induced and organ-specific expression
#cross-references MIID:90151604
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##cross references EMBL:X52179; NID:g20649; PID:g20650
This protein is one of a family of glutamine amidotransferases that have dual specificity to utilize either glutamine or ammonia as a substrate. Two functional domains have been identified: an aminator domain, which catalyzes the ammonia-dependent reaction, and a glutamine amide transfer domain, which binds glutamine and transfers the aminator domain.
                                                                 ##residues 1-586 ##label DOW
##cross-references Explick86489 ND:g669056; PID:g669057
#FICATION #superfamily asparagine synthase (glutamine-h
RDS asparagine biosynthesis; ligase
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Local Similarity 77.8%;
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An asparagine synthetase cDNA clone from Broccoli (Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        asparagine synthetase (glutamine-hydrolyzing)
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#active_site Cys (amide transfer) #status predicted
#th 586 #molecular-weight 66353 #checksum 3350
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  site Cys (amide transfer) **status predicted *molecular-weight 65672 ** **ehecksum 3781
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2; Mismatches (
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31-Dec-1991 #text_change
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Query Match

56.5%;

Score

61; DB

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Length 586

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Best Local Similarity 77.8%;
Matches 7; Conservative
   Query Match 56.5%;
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                                                                                                                                                                                                                                            Clarkson, D.T.

#journal Plant Mol. Biol. (1996) 30:883-897

#title Molecular cloning and characterisation of asparagine synthetase from Lotus japonicus: dynamics of asparagine synthesis in N-sufficient conditions.

#cross-references MID:96270368
                                                                                                                                                                                                                                                                                                                                                #authors
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                                                                                                                                                                                  ##residues
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**residues 1-586 **label WAT
**coss-references EMBL.X89410; NID:g897772; PID:g897773
**experimental_source strain B-129
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#length 586 #molecular-weight 66577 #checksum
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Metabolic regulation of asparagine synthetase gene expression in maize (Zeamays L.) root tips.
                                                                                                                                                                                                                                                                                                                                                                                           Lotus japonicus
#formal_name Lotus japonicus
19-Mar-1997 #sequence_revision 19-Mar-1997
08-Sep-1997
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Score 61; DB 2; I
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Search completed: Fri Jun 11 17:33:46 1999 Job time : 94 secs.

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##experimental_source cv. Nipponbare
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2; Mismatches 0
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************* (ME)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:29:22 1999; MasPar time 2.45 Seconds 172.912 Million cell updates/sec

Tabular output not generated.

Sequence: Description: Perfect Score: >US-08-991-628-4 (1-15) from US08991628.pep 108 1 TPMFLLSRNTGEVRT 15

Scoring table: PAM 150 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 27.687; Variance 32.651; scale 0.848

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Score	Query Match	Length	B G	ID	Description	Pred. No.
108	100.0	999	_ ;	DSG3_HUMAN	DESMOGLEIN 3 PRECURSOR	4.34e-13
88	81.5	1049	ـــ	DSG1_HUMAN	ب	1.08e-07
81	75.0	1043	<u>, , </u>	DSG1_BOVIN	۳	6.60e-06
65	60.2	571	د بــا	ASN1_YEAST	ASPARAGINE SYNTHETASE	4.12e-02
65	60.2	571	_	ASN2_YEAST		4.12e-02
63	58.3	488	_	DSBD_ECOLI	THIOL: DISULFIDE INTERC	1.14e-01
63	58.3	923	-ر	YEL4_YEAST	HYPOTHETICAL 103.3 KD	1.14e-01
61	56.5	524	4	ASNS_SANAU	ASPARAGINE SYNTHETASE	3.06e-01
61	56.5	582	_	ASN2_PEA	ASPARAGINE SYNTHETASE,	3.06e-01
61	56.5	583	ᆫ	ASNS_ARATH	ASPARAGINE SYNTHETASE	3.06e-01
61	56.5	585	<u>, </u>	ASNS_TRIVS	ASPARAGINE SYNTHETASE	3.06e-01
61	56.5	585	-ر	ASNS_BRAOL	ASPARAGINE SYNTHETASE	3.06e-01
61	56.5	. 585	μ	ASNS_MAIZE	ASPARAGINE SYNTHETASE	3.06e-01
61	56.5	585	ب	ASN2_LOTJA	ASPARAGINE SYNTHETASE	3.06e-01
61	56.5	585	Ь	ASN1_PEA		3.06e-01
61	56.5	585	_	ASN1_LOTJA		3.06e-01
61	56.5	590	ட	ASNS_ORYSA	ASPARAGINE SYNTHETASE	3.06e-01
59		589	ـــا	ASNS_ASPOF	ASPARAGINE SYNTHASE [G	8.09e-01
59		1103	<u>بــر</u>	CYGD_HUMAN	RETINAL GUANYLYL CYCLA	8.09e-01
57		171	_	VH01_VARV	PROTEIN-TYROSINE PHOSP	2.08e+00
57		554	ب	ASNB_ECOLI	ASPARAGINE SYNTHETASE	2.08e+00
57	٠	579	ب	DSBD_HAEIN	THIOL: DISULFIDE INTERC	2.08e+00
57	52.8	. 1117	_	DSG2_HUMAN	DESMOGLEIN 2 PRECURSOR	2.08e+00
	Score 108 108 81 65 65 65 66 61 61 61 61 61 61 61 61 61 61 61 61	Que Na en		Query Hength 100.0 999 81.5 1049 75.0 1049 75.0 1049 571 60.2 571 60.2 571 60.2 571 60.2 571 60.5 58.5 58.5 58.5 58.5 58.5 58.5 58.5 5	Watch Length DB 100.0 999 1 100.0 999 1 1043 1 60.2 571 1 60.2 571 1 60.2 571 1 56.5 583 1 56.5 585	Query Match Length DB ID Description 100.0 999 1 DSG3_HUMAN DESMOGLEIN 81.5 1049 1 DSG1_HUMAN DESMOGLEIN 81.5 1049 1 DSG1_HUMAN DESMOGLEIN 81.5 1049 1 DSG1_HUMAN DESMOGLEIN 60.2 571 1 ASN1_YEAST ASPARAGINE 58.3 488 1 DSBD_ECOLI THIOL:DISUI 58.3 923 1 YEL4_YEAST ASPARAGINE 56.5 582 1 ASNS_BANAU ASPARAGINE 56.5 585 1 ASNS_BANAU ASPARAGINE 56.5 585 1 ASNS_BRAOL ASPARAGINE 56.5 585 1 ASNS_DEAT ASPARAGINE 56.5 585 1 ASNS_DEAT ASPARAGINE 56.5 585 1 ASNS_DEAT ASPARAGINE 57.6 1103 1 CYGD_HUMAN PROTEIN-TY 52.8 1117 1 USG2_HUMAN DESMOGLEIN 52.8 1117 1 DSG2_HUMAN DESMOGLEIN

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YLW5_CAEEL FAT_DROME	VIB4_AGRT5	KP78_HUMAN	Y306_MYCPN	MURB_MYCTU	MC5R_BOVIN	LHR_ECOLI	Y089_MYCTU	CGB1_HUMAN	CGB1_MESAU	CGB1_RAT	FD3E_TOBAC	MC5R_MOUSE	MC5R_RAT	FNRA_PSEST	ANR_PSEAE	VE6_HPV03	I12R_HUMAN	CISY_MYCSM	ATPD_RHOBL	YOOH_MYCTU
CADHERIN-RELATED TUMOR	PRECU	PUTATIVE SERINE/THREON	HYPOTHETICAL PROTEIN M	PUTATIVE UDP-N-ACETYLE	MELANOCORTIN-5 RECEPTO	PROBABLE ATP-DEPENDENT	HYPOTHETICAL ABC TRANS	G2/MITOTIC-SPECIFIC CY	G2/MITOTIC-SPECIFIC CY	G2/MITOTIC-SPECIFIC CY	OMEGA-3 FATTY ACID DES	MELANOCORTIN-5 RECEPTO	MELANOCORTIN-5 RECEPTO	TRANSCRIPTIONAL ACTIVA	TRANSCRIPTIONAL ACTIVA	E6 PROTEIN.	INTERLEUKIN-12 RECEPTO	CITRATE SYNTHASE (EC 4	ATP SYNTHASE DELTA CHA	VERY HYPOTHETICAL 14.0
1.28e+0	1.28e+01	1.28e+01	1.28e+01	1.28e+01	1.28e+01	8.22e+00	8.22e+00	5.24e+00	5.24e+00	5.24e+00	5.24e+00									

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41 H D	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	-!- DISEASE: PÉMPHIGUS VULGARIS (PV) IS À POTENTIALLY LETHAL SKIN DISEASE IN WHICH EPIDERNAL BLISTERS OCCUR AS THE RESULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3!- SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS TO THE DESMOSOMAL SUBFAMILY.	-!- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN!- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL, OESOPHAGUS AND CARCINOMAS!- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS	CATARRHINI; HOMINIDAE; HOMO. ROM N.A. 2069753. KLAUS-KOVTUN V., STANLEY J.R.; KCAUS-KOVTUN V., STANLEY J.R.; a disease of cell adhesion."; 9-877(1991).	LT 1 DGG3_HUMAN STANDARD; PRT; 999 AA. P32926; 01-OCT-1993 (REL. 27, CREATED) 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) DESMOGLETIN 3 PRECURSOR (130 KD PEMPHIGUS VULGARIS ANTIGEN) (PVA). DGG3. APIENS (HUMAN). ** EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

SO PETER THE PETER XXX

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Matches
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BUXTON R.S., MAGEE A.I.;
"Desmosomal glycoprotein DGI, a component of intercellular desmo
junctions, is related to the cadherin family of cell adhesion
molecules.";
PROC. NATL. ACAD. SCI. U.S.A. 88:4796-4800(1991).
-i- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS.
INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDI
FILAMENTS MEDIATING CELL-CELL ADBRASION.
-i- SUBCELLULAR LOCATION: TYPE I MEMBRASI PROTEIN.
-i- SUBCELLULAR LOCATION: TYPE I MEMBRASI PROTEIN.
-i- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSILAND OESOPHAGUS.
-i- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
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SEQUENCE
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                                                                                                  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and the modified and this statement is not removed.
                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 91271279.
WHEELER G.N., PARK
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01-NOV-1997
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ISSUE-KERATINOCYTES;
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                                                                           send an email to license@isb-sib.ch).
                                                                                                                                                                                                         (POTENTIAL).
SIMILARITY: BELONGS TO
                                                                                                                                                                                               DESMOSOMAL SUBFAMILY
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                    ; X56654; G30506;
S16906; IJHUG1.
125670; -.
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Similarity 100.0%;
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    PS00232; CADHERIN;
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LAST ANNOTATION UPDATE)
(DESMOSOMAL GLYCOPROTEIN 1)
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CADHERIN 4.
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Pred. No. 4.34e-13
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CYTOPLASMIC (PCCADHERIN 1.
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AE; HOMO.
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                                                                                           (See http://www.isb-sib.ch/announce/
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AND INTERMEDIATE
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CALCIUM-BINDING;
SIGNAL 1
PROPEP 24
CHAIN 50
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MEDLINE; 92037656.
KOCH P.J., GOLDSCH
FRANKE W.W.;
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REPEAT
             SEQUENCE OF 44-493 FROM MEDLINE; 91097553.
                                                                                                                                                                                                                                      MEDLINE; 91168965.

KOCH P.J., WALSH M.J., SCHM
ZIMBELMANN R., FRANKE W.W.;
"Identification of desmogle
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-MUZZLE EPITHELIUM;
KOCH P.J., GOLDSCHMIDT M.D.,
SUBMITTED (MAR-1991) TO EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1993 (REL. 27, C
01-OCT-1993 (REL. 27, L
01-NOV-1997 (REL. 35, L
DESMOGLEIN 1 PRECURSOR
                                                                       "Complete amino acpolypeptide and ide
EUR. J. CELL BIOL.
                                                                                                                                                                                                            glycoprotein, as a
molecules.";
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                                                                                                                                                                                           EUR. J. CELL BIOL.
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METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
*A· RHMINANTIA; PECORA; BOVOIDEA; BOVIDAE
                                                                                                                                   GOLDSCHMIDT M.D.,
HILL J.E., RAYNOR shows extensive ho
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27, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE
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                                           N.A.
                                                                                                                                                                                                                                                                                                                                          M.D., ZIMBELMANN R., FRANKE W.W.; EMBL/GENBANK/DDBJ DATA BANKS.
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Pred. No.
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ogy to
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                                                                                      e epidermal desmoglein precursor
second type of desmoglein gene.";
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MANABE M., COWIN P.; cadherin family of c
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ASN1_YEAST STANDARD; PRT; 571 AA.

P49089;
01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING] 1 (IGUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE 1).

ASPARAGINE SYNTHETASE (BAKER'S YEAST).

SACCHAROYZCES CEREVISTAE (BAKER'S YEAST).

EUKARYOTA; FUNCI; ASCONYCCTA; HEMIASCONYCETES; SACEMARYOTA; FUNCI; ASCONYCETES; SACEMARYOTA; FUNCIPIER 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00028; HSSP; P09803; 1: CELL ADHESION;
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CONFLICT
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EMBL; X57784; G436062; -.
EMBL; M5165; G552318; -.
PIR; S14603; IJBOG1.
PROSITE; PS00232; CADHERIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EPIDERMIS, MUZZLE, TONGUE AND DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE
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SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS TO THE
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DESMOGLEIN REPEAT 2
DESMOGLEIN REPEAT 4
DESMOGLEIN REPEAT 4
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                                                                                                                                                                                                                                                                                                                                                                  Score 81; DB 1; I
Pred. No. 6.60e-06;
5; Mismatches 1
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DESMOGLEIN REI
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CYTOPLASMIC
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EXTRACELLULAR
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13898584 CRC32;
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                                        SACCHAROMYCETALES,
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RESULT REPORT OF SERVICE SERVICES OF SERVI
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Best Local
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JOHNSTON M., ANDERWS S., BRINKMAN R., COODER J., DING H., I
AFAVELLO A., FULTON L., GATTUNG S., GRECO T., KIRSTEN J., KU
HALLSWORTH K., HAWKINS J., HILLIER L., JIER M., JOHNSON D.,
JOHNSTON L., LANGSTON Y., LATREILLE P., LE T., MARDIS E., M
MILLER N., NHAN M., PAULEY A., PELUSO D., RIFKEN L., RILES
A MILLER N., TREVASKIS E., VIGNATI D., MILCOX L., MOHLDMAN P.,
MILSON R., WATERSTON R.;
SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- CATALYTIC ACTIVITY: ATP + L-ASPARATE + L-GLUTAMINE - A
PYROPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE.
-I- PATHWAY: ASPARAGINE BIOSYNTHESIS.
-I- SINILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUTAMI
                                                                                                                                                                                                                                                                                          SULT 5
ASN2_YEAST STANDARD; PRT; 571 AA.
P49090;
01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FOR-1997 (REL. 35, LAST ANOTATION UPDATE)
ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING] 2
ASPARAGINE SYNTHETASE [GLUTAMINE-SYNTHETASE 2).
ASPARAGINE SYNTHETASE (BAKER'S YEAST).
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
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unknown open reading frames, of Ty and three LRNA genes.";
YEAST 13:171-176(1997).
[2]
SEQUENCE FROM N.A.
                                                                                                                       SEQUENCE FROM N.A.
STRAIN-S288C / FY1679;
MEDLINE; 97197982.
VAN DYCK L., TETTELIN H., PURN
"An 18.3 kb DNA fragment from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsit the European Bioinformatics Institute. There are no restrictions
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DANG V.D., BOLOTIN-FUKUHARA M., DAIGNAN-FORNIER
                                                                                                                                                                                                                                                                        SACCHAROMYCETACEAE;
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PFAM; PF00310; GAT
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PFAM; PF00733; Asn_synthase; 1.
LIGASE; ASPARAGINE BIOSYNTHESIS; GLUTAMINE AMIDOTRANSFERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 TPMFLLSRK 354
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PF00733;
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88.9%;
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Pred. No.
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No. 4.12e-02;
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                                                                                                                            VII
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   SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 95334362.
BURLAND V.D., PLUNKET
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-K12 / W3110; MEDLINE; 95349397. FONG S.-T., CAMAKARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSBD_ECOLI STANDARD; PRT; 488 AA.

p36655; P76796;
01-JUN-1994 (REL. 29, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 32, LAST ANNOTATION UPDATE)
THIOL:DISULFIDE INTERCHANCE PROTEIN DSBD (C-TYPE CYTOCHROME BIOGENESIS PROTEIN CYCZ) (INNER MEMBRANE COPPER TOLERANCE PROSED OR CYCZ OR CUTAZ OR DIPZ.

BACTERICHIA COLI.

BACTERICHIA COLI.

BACTERICHIA TROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIA(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CROOKE H., COLE J.;
"The biogenesis of c-type cytochromes membrane-bound protein, DipZ, with a pisomerase-like domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=K12;
MEDLINE; 95349398.
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INIT_MET 0
ACT_SITE 1
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EMBL; 272909; E243463; -.
SGD; L0003156; ASN2.
PROSITE; P800443; GATASE_TYPE_II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- CATALYTIC ACTIVITY: ATP + L-ASPARTATE + L-GLUTAMINE PYROPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE.
-I- PATHMAX: ASPARAGINE BIOSYNTHESIS.
-I- SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUT
                                                                                                                                                                                         FONG S.-T., CAMAKARIS J., LEE B.T.O.;
"MOLECULAR genetics of a chromosomal tolerance in Escherichia coli K-12.";
MOL. MICROBIOL. 15:1127-1137(1995).
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1 TPMFLLSRN 9
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PF00733; Asn_synthase; 1.
E; ASPARAGINE BIOSYNTHESIS; GLUTAMINE AMIDOTRANSFERASE;
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8; Conser
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       PLUNKETT
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88.9%;
       <u>ი</u>
       III,
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Pred. No.
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GATASE (BY SIMILARITY).
; 926C9736 CRC32;
       SOFIA H.J.,
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       DANIELS
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EMBL; U14003; G536980; ALT_
EMBL; AE000486; G1790578; A
EMBL; 236905; G581055; -
PIR; S42064; S42064.
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"Analysis of the I region from 92.8 t
                                                                                            TRANSMEM DOMAIN DISULFID CONFLICT SEQUENCE
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PROSITE;
HSSP; P10
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SAMBONGI Y., FERGUSON S.J.;

Somplement deficiency in c-type cytochrome biogenesis in Escherichia coli carrying a mutation in a membrane-bound disulphide isomerase-like protein.";

FEBS LETT. 353:235-238(1994).

FEBS LETT. 353:235-238(199
                                                                                                                                                                            TRANSMEM DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Identification and characterization of a new isomerase-like protein (DsbD) in Escherichia c EMBO J. 14:3415-3424(1995).
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MISSIAKAS D., HUGHES
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                           h 58.3%;
Similarity. 53.8%;
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through 100 minutes."
s. 23:2105-2119(1995).
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                                                                                            PERIPLASMIC (POTENTIAL)
REDOX-ACTIVE (BY SIMILA
L -> V (IN REF. 1).
FE6A2C9F CRC32;
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                              Mismatches
                                              63; DB 1;
No. 1.14e-01
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                                                           DB 1;
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Matches 7; Conse
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DIETRICH F.S., MULLIAN J.T., HENNESSEY K.M., ALLEN E., ARAUJO R.,
AVILES E., BERNO A., BRENNAN T., CARPENTER J., CHEN E., CHERRY J.M.
CHUNG E., DUNCAN M., GUZMAN E., HARTZELL G., HUNICKE-SMITH S.,
HYMAN R., KAYSER A., KOMP C., LASHKARI D., LEW H., LIN D.,
MOSEDALE D., NAKAHARA K., NAMATH A., NORGREN R., OEFNER P., OH C.,
PETEL F.X., ROBERTS D., SEHL P., SCHRAMY S., SHOGREN T., SMITH V.,
TAYLOR P., WEI Y., YELTON M., BOTSTEIN D., DAVIS R.W.;
SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-1- SIMILARITY: BELONGS TO THE CARNITINE/CHOLINE ACETYLTRANSFERASE
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (REL. 3)
01-FEB-1995 (REL. 3)
01-FEB-1995 (REL. 3)
HYPOTHETICAL 103.3 1
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the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
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P40017;
                                                                                                                                                                                                                                                                                                                                                         ASNS_SANAU STANDARD; PRT; 524 AA. 024338; 15-DEC-1998 (REL. 37, CREATED) 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE) 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) ASPARAGINE SYNTHETASE (GLUTANINE-HYDROLYZING)
EASON J.R., KING G.A.;
"Nucleotide sequence of cDNA encoding asparagine
"andersonia aurantiaca.";
(IN) PLANT GENE REGISTER PGR97-112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content
                                                                                                                                                                                                                                SANDERSONIA AURANTIACA (CHRISTMAS-BELLS)
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; 1
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMY
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PROSITE; PS00440; ACYLTRANSE_C_2; 1
PFAM; PF00755; CATD_ACYLTRANSE; 1.
HYPOTHETICAL PROTEIN; TRANSFERASE;
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                                                                                                                                                      SEQUENCE FROM N.A.
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Pred. No. 1.14e-01
4; Mismatches
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                                                                                                                                                                                                                                                              EMBRYOPHYTA;
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EMBRYOPHYTA; TRACHEOPHYTA;
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Best Local Similarity
Matches 7; Consei
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*Park-induced a...

*Synthetase genes in Pisum sa...

EMBO J. 9:323-332(1990).

-i- CATALYTIC ACTIVITY: ATP + L-ASPARTATE +

-i- CATALYTIC ACTIVITY: ATP + L-ASPARAGINE + L-GLUTAMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INIT_MET
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  ASN2_PEA
P19252;
                                                                                                                                                                                                                                                                                                                                                      01-NOV-1990 (REL. 16, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
ASPARAGINE SYNTHETASE, ROOT [GLUTAMINE-HYDROLYZING]
(GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                               This
                                                                                                                                                                                                                                                                                                         PISUM SATIVUM (GARDEN PEA).
EUKARYOTA; VIRIDIPLANTAE; STREI
EUPHYLLOPHYTES; SPERMATOPHYTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF005724; G2245622; PROSITE; PS00443; GATASE_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                            'Dark-induced and organ-specific expression of two ynthetase genes in Pisum sativum.";
                                                                                                                                                                                                                                    MEDLINE; 90151604
TSAI F.Y., CORUZZ
                                                                                                                                                                                                                                                                                              ABALES;
                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGASE;
                                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
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                                                                                                                                            PATHMAY: ASPARAGINE + L-GLUTAMATE.
TISSUE SPECIFICITY: ROOTS.
INDUCTION: name-in-
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                                                                                                                              INDUCTION: DARK-INDUCED
SIMILARITY: THE GATASE I
                                                                                                       SIMILARITY:
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PATHWAY: ASPARAGINE BIOSYNTHESIS
                                                                                                                   AMIDOTRANSFERASES
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                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y., CORUZZI G.M.;
                                                                                                                                                                                                                                                             SPARKLE;
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                                                                                                       OTHER ASN SYNTHETASES.
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SPARAGINE + L-GLUTAMATE.
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Mismatches (
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PHYTA; EUDICOTYLEDONS; ROSI
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CRC32;
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PROSITE; PS00443; GATASE_TYPE_II;

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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entitles requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Metabolic regulation of the gene encoding glutamine-dependent asparagine synthetase in Arabidopsis thaliana.";
PLANT PHYSICL 106:1347-1357(1994).

-:- CATALYTIC ACTIVITY: ATP + L-ASPARTATE + L-GLUTAMINE = AMP + DYROPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE.

-:- PATHWAY: ASPARAGINE BIOSYNTHESIS.

-:- SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUTAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARXOTA; VIRIDIPLANTAE; STREPTOPHYTA; EUBRYOPHYTA; TRACHEOPHYTA;
EUPRYLLOPHYTES; SPERNATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSI
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00310; GATase_2; 1. PFAM; PF00733; Asn_synthase;
                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00443; GATASE_TYPE_II;
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between
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                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                              MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAM H.M., PENG S.S., CORUZZI G.M.;
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                         321 TPMFLMSRK 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the El
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L29083; G507946; -
                                                                                                                                                                                                                                                                                                                                                PF00310;
                                                                                                 Similarity
                                                                                                                                                                                                                                                                        ASPARAGINE BIOSYNTHESIS; GLUTAMINE AMIDOTRANSFERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                               an email to license@isb-sib.ch).
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GATASE (BY SIMILA
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GATASE (BY SI
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Matches 7; Conse
                                                           ASNS_BRAOL STANDARD; PRT; 585 AA. P49091; 01-FEB-1996 (REL. 33, CREATED) 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) ASPARAGINE SYNTHETASE; GLUTAMINE-HYDROLYZING] DEPENDENT ASPARAGINE SYNTHETASE).
BRASSICA OLERACEA (CAULLIFLOWER).
BRASSICA OLERACEA (CAULLIFLOWER).
                                                                                                                                                                                                                                                                                                                                                           INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entitles requires a license agreement (see http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Host root exudate increases expression of asparagine synthetic the roots of a hemiparasitic plant Triphysaria (Scrophulariace SUBMITTED (SEP-1997) TO EMBL/GENBANK/DIBJ DATA BANKS.

-I- CATALYTIC ACTIVITY: ATP + L-ASPARATATE + L-GLUTAMINE - AMP PYROPHOSPHATE + L-ASPARATINE + L-GLUTAMATE.

-I- PATHMAY: ASPARAGINE BIOSYNTHESIS.

-I- SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUTAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRIPHYSARIA VERSICOLOR.
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA;
TRACHEOPHYTA; EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA;
EUDICOTYLEDONS; ASTERIDAE; GENTIANANAE; LAMIALES; SCROPHULARIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               024661;
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                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF014055; G2429280; -.
EMBL; AF014056; G2429282; -.
EMBL; AF014057; G2429284; -.
PROSITE; PS00443; GATASE_TYPE_II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEPENDENT ASPARAGINE SYNTHETASE).
                                         EUKARYOTA; VIRIDIPLANTĀE; STREPTOPHYTA; EMBRY
EUPHYLLOPHYTES; SÆRMĀTOPHYTA; MAGNOLIOPHYTA;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (REL. 37,
ASPARAGINE SYNTHETASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998
15-DEC-1998
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 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00310; GATase_2; 1.
PFAM; PF00733; Asn_synthase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISSUE-ROOT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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SIMILARITY: TO OTHER ASN SYNTHETASES.
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                                                                                                                                                                                                                                                                                                                                          BIOSYNTHESIS; GLUTAMINE AMIDOTRAN
0 BY SIMILARITY.
1 GATASE (BY SIMILARITY).
65560 MW; B3ACC66E CRC32;
                                                                                                                                                                                                                                                                                                  56.5%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
[GLUTAMINE-HYDROLYZING]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CREATED
                                                                                                                                                                                                                                                                                                  Score 61;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                       GLUTAMINE AMIDOTRANSFERASE
                                                                                                                                                                                                                                                                                                    DB 1;
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                                                        EMBRYOPHYTA;
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                                           EUDICOTYLEDONS;
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aragine synthetase
(Scrophulariaceae)
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                                                                                                 6.3.5.4) (GLUTAMINE:
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                                                         TRACHEOPHYTA;
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Best Local
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ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING]
DEPENDENT ASPARAGINE SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV. DEA; TISSUE-ROOT MEDLINE; 96158342.
CHEVALIER C., BOURGEOIS E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ÷
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DOWNS C.G., POGSON B.J., DAVIES K.M., ALMIRA E.C.;
"An asparagine synthetase cDNA clone from Broccoli (Brassica oleracea
                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZEA MAYS (MAIZE).
EURARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASNS_MAIZE P49094;
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O BY SIMILARITY.

O GATASE (BY SIMILARITY).

SEQUENCE 585 AA; 65541 MW; B6DCFB50 CRC32;

    -!- SIMILARITY: TO OTHER ASN SYNTHETASES.

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PARHWAY: ASPARAGINE BIOSYNTHESIS.
SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUTAM
                                                                                                                                                                                                             SIMILARITY: TO OTHER ASN SYNTHETASES.
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Similarity 77.8%;
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-ROOT MERISTEM
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Pred. No.
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Ouery Match 56.58
Best Local Similarity 77.88
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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MAIZEDB; 79071; -.

PROSITE; PS00443; GATASE_TYPE_II; 1.

PFAM; PF00310; GATase_2; 1.

PFAM; PF00733; Asn_synthase; 1.

LIGASE; ASPARAGINE BIOSYNTHESIS; GLUTAMINE AMIDOTRANSFERASE.

INIT_MET 0 BY SIMILARITY.

ACT_SITE 1 1 GATASE (BY SIMILARITY).

SEQUENCE 585 AA; 66446 MW; B24B0478 CRC32;
                                                                                                                                                                                                                                                                                                                                                                             CONDITIONS.;

PLANT MOL. BIOL. 30:883-897(1996).

-I- CATALYTIC ACTIVITY: ATP + L-ASPARTATE + L-GLUTAMINE
PYROPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE.

-I- PATHWAY: ASPARAGINE BIOSYNTHESIS.

-I- SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUTAMIDOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING]
(GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASN2_LOTJA
P49093;
                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                    PFAM; PF00310; GATase_2; 1.
PFAM; PF00733; Asn_synthase; 1.
HSSP; P17169; 1GMS.
LIGASE; ASPARAGINE BIOSYNTHESIS;
                                                                                                                                                                                   EMBL; X89410; G897773; -.
PROSITE; PS00443; GATASE_TYPE_II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. GIFU / B-129;
MEDLINE; 96270368.
WATERHOUSE R.N., SMYTH A.J.,
CLARKSON D.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FABALES; FABACEAE; PAPILIONOIDEAE; LOTUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSI
                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: TO OTHER ASN SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                           INIT_MET
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning and characterisation
Lotus japonicus: dynamics of asparagine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOTUS JAPONICUS
                                                                                                           MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 TPMFLMSRK 329
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                                                            585 AA;
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77.8%;
                56.5%;
77.8%;
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 Score 61; DB 1; I
Pred. No. 3.06e-01;
2; Mismatches C
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Pred. No. 3.06e-01;
2; Mismatches 0
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                                                            BY SIMILARITY.
GATASE (BY SIMILARITY)
; 2FE40574 CRC32;
                                                                                                                         GLUTAMINE AMIDOTRANSFERASE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of asparagine synthesis in N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 585
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                                Length 585;
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Search completed: Fri Jun 11 17:29:30 1999 Job time : 8 secs.
                                                                                                            Query Match 56.5%;
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                      MULTIGENE INIT_MET ACT_SITE SEQUENCE
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PRT: 585 AA.

219251;
01-NOV-1990 (REL. 16, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
ASPARAGINE SYNTHETASE, NODULE [GLUTAMINE-HYDROLYZING] (EC.6.3.5.4)
(GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X52179; G20650; -.
PIR; S11444; AJPMN1
PROSITE; P500443; GATASE_TYPE_II; 1.
PFAM; PF00310; GATASe_2; 1.
PFAM; PF00733; ASn_synthase; 1.
HSSP; P17169; IGMS.
HSSP; ASPARAGINE BIOSYNTHESIS; GLUTAMINE AMIDOTRANSFERASE;
                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CV. SPARKLE; TISSUE-ROOT NODULES;
MEDLINE; 90151604.
TSAI F.Y., CORUZZI G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PISUM SATIVUM (GARDEN PEA).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYTLOPHYTES; SPERWATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
FABALES; FABACEAE; PAPILIONOIDEAE; PISUM.
                                                      322 TPMFLMSRK 330
|||||:||:
1 TPMFLLSRN 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 TPMFLMSRK 329
||||:||:
| 1 TPMFLLSRN 9
                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  · ! - SIMILARITY: TO OTHER ASN SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMIDOTRANSFERASES.
                                                                                                                                                                                                                  FAMILY.
                                                                                                                                                                        585 AA;
                                                                                                                                                                        66222 MW;
                                                                                                                                                                                              0 ب
                                                                                                             Score 61; DB 1; Length 585;
Pred. No. 3.06e-01;
2; Mismatches 0; Indels
                                                                                                                                                                     BY SIMILARITY.
GATASE (BY SIMILARITY).
; 9AB4FBC5 CRC32;
                                                                                                             0
                                                                                                             Gaps
                                                                                                               0
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********* (MT)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:29:48.1999; MasPar time 6.28 Seconds 130.422 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-991-628-4 (1-15) from US08991628.pep 108 1 TPMFLLSDAMFOLE

Scoring table: PAM 150 Gap 15

Searched: 179066 segs, 54579741 residues

bost-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl9
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
1:sp_archea 2:sp_bacteria 7:sp_mhc 8:sp_organelle
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Mean 27.267; Variance 32.331; scale 0.843

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

14 116 117 118 20	10 11 13	7654	Result No.
ល	1 4 4 6 6 8 1 1 4 4 6 6 8 1	60110 600 600 600 600 600 600 600 600 60	Score 90
51.9 51.9 50.9			CP.
300 496 579 1 579 1 501 1	586 586 1486 1486 1486 1486 1486 1486 1486 14	581 581 1	H 10
0 04992 2 069782 1 058705 0 P93168 0 Q42792 2 050455 3 P87358	0 024483 0 P93618 0 Q40328 0 058871 1 058871 4 015039	2 Q04824 2 Q04824 5 Q20732 5 Q20732 3 Q42902 0 P93167 0 P93167	;
DAPA. DAPA. 496AA LONG HYPOTHETICA 496AA LONG HYPOTHETICA ASPARAGINE SYNTHETASE ASPARAGINE SYNTHETASE PUTATIVE MAGNESIUM AND ZNR-1.	ASPARAGINE SYNTHETASE ASPARAGINE SYNTHETASE ASPARAGINE SYNTHETASE. 148AA LONG HYPOTHETICA KIAA0327 PROTEIN. RIBONUCLEOTIDE REDUCTA	H b	(FRA
3.79e+00 02A 6.05e+00 6.05e+00 E 6.05e+00 9.59e+00 9.59e+00		י על	- 5 F

4 .5	44	43	42	41	40	39	38	37	36	ა ა	34	ω ω	32	ω	30	29	28	27	26	25	24	23	22	
52	5 3	53	53	53	53	5 3	53	53	53	53	5 3	53	5 ω	54	54	54	54	54	54	54	54	54	54	
48.1	49.1	49.1	49.1	49.1	49.1	49.1	49.1	49.1	49.1	49.1	49.1	49.1	49.1	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	
326	1607	1468	1220	1163	814	736	578	453	433	393	373	319	215	1919	1807	792	762	610	309	244	244	170	163	
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Q18666	Q94599	067762	Q98864	018820	064681	024816	P72723	Q22370	041107	008395	Q49979	086864	044017	042998	013661	075278	P96793	077330	001259	085222	044500	Q29035	084262	
C47D12.3 PROTEIN.	LCFACAS5.	RNA POLYMERASE BETA SU	PATCHED PROTEIN.	SIMILARITY TO INSULIN	F22013.35.	POLYPHOSPHATE KINASE.	POTENTIAL FMN-PROTEIN.	T10B10.2 PROTEIN.	A625R PROTEIN.	CITRATE SYNTHASE (EC 4	CORA.	STRT.	ERD2 GENE.	HYPOTHETICAL 217.7 KD	HYPOTHETICAL 229.9KD P	KIAA0345-LIKE 2.	XYLQ.	MAL3P3.14 PROTEIN.	T20D3.8 PROTEIN.	ANAEROBIC REGULATORY P	CYTOCHROME BD.	CYCLIN B (FRAGMENT).	HYPOTHETICAL 18.9 KD P	
3.67e+01	2.36e+01	2.36e+01		2.36e+01	2.36e+01	2.36e+01		2.36e+01	2.36e+01	2.36e+01	2.36e+01	2.36e+01	2.36e+01	1.51e+01	1.51e+01	1.51e+01	1.51e+01	1.51e+01	1.51e+01	1.51e+01	1.51e+01	1.51e+01	1.51e+01	

ALIGNMENTS

000000000000000000000000000000000000000	Qy RESULT	¥ # 6	SQ SQ	\$ \$ \$ \$ \$ \$ \$ \$	188888	3555	RESULT
01-NOV-1996 (TREMBLREL. 01, CREATED) 01-NOV-1996 (TREMBLREL. 01, LAST SCOUGHNCE UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) HYPOTHETICAL 37.7 KD PROTEIN 2K177.6 IN CHROMOSOME II. 2K177.6. 2K177.6. CAENORHABDITIS ETEGANS. CAENORHABDITIS ETEGANS. EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.	207 SMFLISRNTGEVRT 220 : : 2 PMFLLSRNTGEVRT 15	Query Match 83.3%; Score 90; DB 11; Length 993; Best Local Similarity 85.7%; Pred. No. 5.59e-08; Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	PROSITE; PS00232; CADHERIN; 2. PRAM; PF00028; CADHERIN; 4. CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; CALCIUM-BINDING; REPEAT. NON TER 993 993 SEQUENCE 993 AA; 107888 MW; 881794BD CRC32;	9 H	MUSCULI ARYOTA; UROGNATI	8 (TREMBLREL. 8 (TREMBLREL. 8 (TREMBLREL.	LT 1 O35902 PRELIMINARY; PRT; 993 AA.

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AC 202732:
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DT 01-NOV-1996 (
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CAENOHARABDIT (
CAENOHARABDIT (
CAENOHARABDIT (
RN [1]
RP SEQUENCE FROM
RA WILKINSON J.;
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Best Local
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Best Local
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01-NOV-1996 (TREMBLREL 01, L
01-JAN-1999 (TREMBLREL 09, L
ORF6 PROTEIN PRECURSOR.
SALMONELLA TYPHIMURIUM.
PLASMID 90 KB VIRULENCE.
BACTERIA; PROTEOBACTERIA; GAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q04824
Q04824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAINLTZ;
MEDLINE; 93316852.
FRIEDRICH M.J., KINSEY N.E., VILA J
"Nucleotide sequence of a 13.9 kb s
plasmid of Salmonella typhimurium:
                                                                                                                                                                                                  CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITI
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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MOL. MICROBIOL. 8:543-558(1993).
EMBL; L08613; G154246; -
   SEQUENCE FROM N.A MEDLINE; 94150718
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 PMFTIDEHTGOVRT
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8; Conservative
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                                                                                      J.;
(JUL-1996)
                                                                                                                                                                                                                                                                                                                    (TREMBLREL.)
(TREMBLREL.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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30683 MW;
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57.1%;
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                                                                                      EMBL/GENBANK/DDBJ
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                                                                                                                                                                                                                                                                                                                    CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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ORF6 PROTEIN.
; C4D5ADDF CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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1.22e-01;
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                                                                                      DATA
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Best Local
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elegans.";
NATURE 368:32-38(1994).
EMBL; 277664; E255929; -.
PFAM; PF00092; VWa; 1.
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Best Local
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                                                                                                                                                                                                          01-MAY-1997 (TREMBLREL. 03, 01-MAY-1997 (TREMBLREL. 03, 01-JAN-1999 (TREMBLREL. 09) ASPARAGINE SYNTHETASE 2 (EC (GLUTAMINE-HYDROLYSING)) (A (GLUTAMINE-HYDROLYSING)).
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BONFIELD J., BURTON J. CONNELL M., COPSEY T., COOPER J.,
CRAXTON M., DEAR S., DU Z., DURBLIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER L., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 M of contiguous nucleotide sequence from chromosome III of C
                                                                                                                                                                                                                                                                                                                                                                                  LT 6
P93167
                                                                                                                 GLYCINE MAX (SOYBEAN).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHEUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
SEQUENCE FROM N.A. STRAIN-CENTURY; TISSUE-MATURE LEAF MEDLINE; 97188563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-972H-;
WOOD V., RAJANDREAM M.A., BARRELL B.G., SKELTON J., (
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; AL022117; E1263968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
ASPARAGINE SYNTHETASE.
                                                                                             FABALES; FABACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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larity 77.8%;
Conservative
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                                                                                           PAPILIONOIDEAE;
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                                                                                                                                                                                                                              . 03, CREATED)
. 03, LAST SEQUENCE UPDATE)
. 09, LAST ANNOTATION UPDATE)
2 (EC 6.3.5.4) (ASPARAGINE SYNT)
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Pred. No. 5.50e-01;
2; Mismatches 0;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 3.35e-01;
2; Mismatches 4
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024483;
024483;
01-JAN-1998 (TREMBLREL. 01-JAN-1998 (TREMBLREL. 01-NOV-1998 (TREMBLREL. ASPARAGINE SYNTHETASE.
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01-AUG-1998
01-AUG-1998
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065329;
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"Molecular cloning and expression of two cDNA
synthetase in soybean.";
PLANT MOL. BIOL. 33:301-311(1997).
-!- CATALYTIC ACTIVITY: ATP + L-ASPARTATE + L
DIPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE.
EMBL; U77678; G1778370; -.
                                an asparagine synthetase gene showing nodules and dark-adapted leaves."; PLANT CELL 9:1339-1356(1997).
EMBL; U89923; G2522320; -.
                                                                                                                    SHI L., TWARY S.N., YOSHIOKA H., GREGERSON R.G., MILLER S.S., SAMAC D.A., GANTI J.S., UNKEFER P.J., VANCE C.P.; "Nitrogen assimilation in alfalfa: isolation and characterization an asparagine synthetase gene showing enhanced expression in root
                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 97432147. SHI L., TWARY S.N.
                                                                                                                                                                                                                                                                                                                                                                   MEDICAGO SATIVA (ALFALFA).
EUKARYOTA; VIRIDIPLANTAE; STREI
EUPHYLLOPHYTES; SPERMATOPHYTA;
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EUKARYOTA; VIRIDIPLANTAE; STRE
EUPHYLLOPHYTES; SPERMATOPHYTA;
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LIGASE.
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E SYNTHETASE.
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                                                                                                                                                                                                                                                                                                                                      LANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; ERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSI PAPILIONOIDEAE; MEDICAGO.
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77.8%;
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Pred. No.
2; Misma
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LAST SEQUENCE UPDATE)
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Pred. No. 5.50e-01
2; Mismatches
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5.50e-01;
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Query
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                                  SUBMITIED (FEB-1996) TO EMBL/GEI
EMBL; L40327; G1184265; -.
PFAM; PF00310; GATase_2; 1.
PFAM; PF00733; Asn_synthase; 1.
MENDEL; 9036; MEDga; 1042; 1.
SEQUENCE: 586 AA; 66462 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1997
01-MAY-1997
01-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                   LT 10
Q40328
Q40328;
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P93618;
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SEQUENCE
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STRAIN-KLEINE THEERINGER; TISSUE-ROOT NODULE;
STRAIN-KLEINE THEERINGER; TISSUE-ROOT NODULE;
                                                                                                                                                                                                                                               MEDICAGO SATIVA (ALFALFA).
EUKAKYOTA; VIRIDIPLANTAE; STREPTOPI
EUPHYTLOCHYTES; SPERMATOPHYTA; MAGI
FABALES; FABACEAE; PAPILIONOIDEAE;
                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-JAN-1999 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VICIA FABA (BROAD BEAN).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERWATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSI
FABALES; FABACEAE; PAPILIONOIDEAE; VICIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00733;
SEQUENCE 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KUESTER H., ALBUS U., FRUEH:
PUEHLER A., PERLICK A.M.;
PLANT SCI. 124:89-95(1997).
-I- CATALYTIC ACTIVITY: ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GANTT S.;
                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    ASPARAGINE SYNTHETASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1997 (TREMBLREL. 03, CREATED)
01-WAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-VAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
ASPARAGINE SYNTHETASE (EC 6.3.5.4) (ASPARAGINE SYNTHASE
(GLUTAMINE-HYDROLYSING)) (ASPARAGINE SYNTHETASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 TPMFLMSRK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLUTAMINE-HYDROLYSING)).
Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00310;
PF00733;
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                                                                                                                                                                                       SARANAC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Asn_synthase;
VICfa;1042;1.
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AA; 66448 MW;
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77.8%;
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77.8%;
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56.5%;
                                                                                                                                               TO EMBL/GENBANK/DDBJ
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HYTA; MAGNOLIOPHYTA; EUDICO
DNOIDEAE; MEDICAGO.
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Pred. No.
2; Misma
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Pred. No.
2; Misma
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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E + L-GLUTAMATE.
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                                         962C3A3F
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61;
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5.50e-01;
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10;
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Length 586;
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05887];
01-AUG-1998 (TREMBLREL. 07
01-JAUG-1998 (TREMBLREL. 07
01-JAN-1999 (TREMBLREL. 07
148AA LONG HYPOTHETICAL P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998
01-JAN-1998
01-NOV-1998
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015039;
                                                                                                                                                                                                                                                                                                                                                                           NAGASE T., ISHIKAWA K., NAKAJIMA D., OHIRA M., SEKI
TANAKA A., KOTANI H., NOMURA O.;
"Prediction of the coding sequences of unidentified
The complete sequences of 100 new cDNA clones from k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete Sequence and Gene Organization of the Genome of a Hyper-thermophilic Archaebacterium, Pyrococcus horikoshii OT3."; DNA RES. 5:55-76(1998).
EMBL; APO00005; D1031206; -. SEQUENCE 148 AA; 17401 MW; 6B16BC02 CRC32;
                                                                                                PFAM; PF00028; cadherin; 6.
CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; CALCIUM-BINDING; SEQUENCE 820 AA; 89864 MM; 3B6ECA92 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVNARASALI I., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI
AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA
KIKUCHI H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAWARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y., YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y., SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y., SAKAI M., OGURA K., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI
                                                                                                                                                                                                DNA RES. 4:141-150(1997).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE EMBL; AB002325; D1021623; -.
PROSITE; PS00232; CADHERIN; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYROCOCCUS HORIKOSHII.
ARCHAEA; EURYARCHAEOTA;
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ES. 4:141-150(1997).
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(TREMBLREL.)
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07, LAST SEQUENCE UP
09, LAST ANNOTATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 59;
Pred. No.
3; Misma
Score
Pred.
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2; Mismatches 0;
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No.
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   DB 4; I
1.46e+00;
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01-JUN-1998
01-AUG-1998
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049927
                                                                                                                                                                     SEQUENCE FROM N.A.

CASTILLO J., MARQUEZ J.A., FRANCO L., BALLESTAR E., F SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

EMBL; Y11207; E321874; -.

SEQUENCE 483 AA; 54662 MW; D4481891 CRC32;
                                                                                                                                                                                                                                                                                              PISUM SATIVUM (GARDEN PEA).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYTLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSI
FABALES; FABACEAE; PAPILIONOIDEAE; PISUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA EMBL; U75930; G1911278; -. PFAM; PFOM317; ribonucleo_red; 1. SEQUENCE 593 AA; 65952 MW; OB19B9ED CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIBONUCLEOTIDE REDUCTASE LARGE SUBUNIT.
ORGYIA PSEUDOTSUGATA NUCLEAR POLYHEDROSIS VIRUS.
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; BACULOVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1997 (TREMBLREL.
01-JUL-1997 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The sequence of the Orgyia polyhedrosis virus genome."; VIROLOGY 229:381-399(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. ROHRMANN G.F.;
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llarity 50.0%;
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2.36e+00;
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RESULT 15
10 069782;
AC 069782;
DT 01-AUG-1998 (TREMBLEEL 07, CREATED)
DT 01-AUG-1998 (TREMBLEEL 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLEEL 07, LAST ANNOTATION UPDATE)
DT 01-AUG-1999 (TREMBLEEL 07, LAST ANNOTATION UPDATE)
DAPA.

GN DAPA.

GN DAPA.
OS SINORHIZOBIUM MELILOTI.
OC BACTERIA, PROTEODRACTERIA, ALPHA SUBDIVISION, RHIZOBIACEAE GROUP;
OC RHIZOBIACEAE, SINORHIZOBIUM.

RN SEQUENCE FROM N.A.

RC STRAIN-CR4;
RA ZERRI S., GARCIA-RODRIGUEZ F., TORO N.;
RN SUBNITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RMS ZERRI S., GARCIA-RODRIGUEZ F., TORO N.;
RN SUBNITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RMS ZERRI S., GARCIA-RODRIGUEZ F., TORO N.;
RN SUBNITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RMS ZERRI S., GARCIA-RODRIGUEZ F., TORO N.;
RN SUBNITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RMS ZERRI S., GARCIA-RODRIGUEZ F., TORO N.;
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RMS ZERRI S., GARCIA-RODRIGUEZ F., TORO N.;
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RN SUBNITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RMS ZERRI S., GARCIA-RODRIGUEZ F., TORO N.;
RN SUBNIT TORO
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:43:07 1999; MasPar time 4.85 Seconds
65.749 Million cell updates/sec

Tabular output not generated.

Title: >US-08-991-628-5
Description: (1-15) from US08991628.pep
Perfect Score: 113

Sequence: 1 CECNIKVKDVNDNFP 15

Scoring table: PAM 150 Gap 15

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35 1:part1 2

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38 39:part39

Statistics: Mean 18.398; Variance 59.622; scale 0.309

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	- 194 - 194	Length	S B	ID	cription
21	113 113	100.0	15 999	6	W04845 R30742	Self epitope of desmo Human pemphiqus vulga
w	102	90.3	614	19	W07908	н
4	89	78.8	778	21	W15489	Pemphigus foliaceus a
ທ	72	63.7	787	17	R86865	Human protocadherin p
σ	57	50.4	780	24	W25634	Human cadherin-5.
7	57	50.4	780	21	W13130	Full length human cad
œ	56	49.6	83	39	W84311	Oryza sativa sequence
9	56	49.6	1822	10	R55273	Beta subunit of integ
10	54	47.8	43	11	R58865	Rat-224 cadherin part
11	54	47.8	43	17	R87107	Protocadherin clone R
12	53	46.9	83	29	W55470	H. pylori ORF 06apl11
13	53	46.9	87	29	W55280	ORF
14	52	46.0	11	21	W13139	Human cadherin-5 anti
15	52	46.0	132	w	R13947	E47 cDNA prod. (pE47P
16	52	46.0	162	w	R14626	

45	44	3	42	41	40	39	38	37	36	<u>3</u> 5	34	w w	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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Ψ	R13251	w	R13946	R94892	W37908	W37907	R94891	W13010	P82052	W73630	W00384	R85856	W55048	W38510	W13126	W25639	W25635	W13132	W13127	W25640	R87117	R58875	R38889	W61273	R72798	31	R93190	880280
Drosophila FRU 2 poly		agment (cDNA prod.	1 fragment (domai	5-Pfs28C f	Tbv25-Pfs28B fusion p	ragment	Segment of desmosomal	25 kD surface antigen	g o	Plasmodium falciparum			Streptococcus pneumon	w.		-	Full length human cad	Truncated rat cadheri	Rat truncated cadheri	Protocadherin clone R	n par	encoded by	Homo sapiens protocad		Variant beta-lactoglo		Ethyl esterified boyl
	3.05e+02				:	0	.0	:	.05e+0	.05e+0	.44e+0	.44e+0	2.44e+02	.44e+0	.96e+0	.96e+0	.96e+0	.96e+0	.96e+0	.96e+0	.96e+0	:_	.56e+0	.56e+0	•	1.56e+02	.56e+	. Doe+o

ALIGNMENTS

RESULT

auto-immune disease Claim 1; Page 40; 58pp; English. Chaim 1; Page 40; 58pp; English. Pharmaceutical preparations for tolerisation to antigens comprise either an isolated human non-collagen or non-myslin basic protein (MBP) polypeptide which is capable of tolerising an individual to autoantigen; or an isolated human pathogen polypeptide capable of tolerising an individual to that polypeptide. In both cases, the

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RESULT RESULT DIT RESU
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30-JUN-1995; 165632.
30-JUN-1994; JP-173291.
(NISH) NISHUKAWA T
WPI; 96-388562/39.
                                                                                                                                        Fused protein recognised by pemphigus vulgaris auto:antibody useful to treat and diagnose pemphis vulgaris Claim 1; Page 7-9; 9pp; Japanese.

W07908 represents the human pemphigus vulgaris (PV) antigen extracellular region. The PV antigen is produced in patients wit pemphis vulgaris resulting in autoimmune disease. PV is a rare relapsing disease causing suprabasal, intra-epidermal bullae (vesicles) of the skin and mucuous membranes, which is fatal if untreated. The PV antigen was fused to a human IgGl hinge region and the resulting fusion protein is useful to treat or diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding pemphigus vulgaris antigen - useful in proteins for diagnostic and therapeutic uses Disclosure; Fig 7; 50pp; English. This sequence is the pemphigus vulgaris 130kD antigen. The protein and its encoding DNA may be used in the diagnosis and treatment of pemphigus vulgaris. It is thought that the antigen may be a cell adhesion molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amagai M,
WPI; 93-06
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Pemphigus vulgaris antigen protein extracellular region.
Pemphigus vulgaris antigen protein extracellular region.
Putoantibody; immunoglobulin G; IgGl; fusion protein; diagnosis;
treatment; pemphigus vulgaris; PV; bulla; blister; skin disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
J08188540-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; Q35992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pemphigus vulgaris; skin disease; e
keratinocyte cell surface antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T 2
R30742 standard;
                                                                                                                           pemphigus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dermatology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W07908
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(USSH ) US DEPT HEALTH &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-NOV-1991; 798918
27-NOV-1991; US-798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JUN-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 cecnikvkdvndnfp 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.0%;
hes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ب
                                                                                                 the resulting fusion phigus vulgaris. uence 614 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             μ
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93-067436/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pemphigus vulgaris 130kD antigen.
igus vulgaris; skin disease; autoantibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
       Similarity
14; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 100.0%;
Similarity 100.0%;
15; Conservative
  90.3%;
larity .93.3%;
Conservative
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V, Stanley JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              999
Score 102; DB 19;
Pred. No. 6.20e-04;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 113;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 3.31e-05; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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3.31e-05;
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                                              Length 614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell adhesion
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                                                                                                                                             hinge region
or diagnose
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pemphigus foliaceus antigen-IgG constant region fusion protein - linked through the hinge region used to treat pemphigus foliaceus Claim 1; Page 10:12; 17pp; Japanese.

This sequence represents a fused protein recognised by pemphigus foliaceus patient autoantibody which comprises the constant region of IgG linked to the extracellular region of pemphigus foliaceus is antigen protein through the hinge portion. Pemphigus foliaceus is antigen protein through the hinge portion. Pemphigus foliaceus is a chronic, generalised, vesicular and scaling skin eruption similar to dermatitis herpetiformis. The pemphigus foliaceus antigen fusion protein is useful to treat pemphigus foliaceus. The antigen is especially administered through an adsorbent upon which the fusion protein is immunobilised via a carrier. The fusion protein is also useful for detecting pemphigus foliaceus antibodies which is useful immunodiagnosis. The fusion protein has little or no side effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                   04-JAN-1996.
26-JUN-1995; U08071.
27-JUN-1994; US-268161.
(DOHE-) DOHENY EYE INST
Suzuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-1997.
12-SEP-1995; 260899.
12-SEP-1995; JP-2608
(NISH/) NISHIKAWA T.
WPI; 97-241758/22.
Polynucleotide(s) encoding human protocadherins pc3 and pc4 and rat pc5 - involved in cell-cell adhesion and regulation activities Claim 15; Page 115-119; 146pp; English.

R86865-R86867 represent the sequences for three protocadherins. Th sequence represents the human protocadherin pc3. These sequences a related to cadherin, and possess cell adhesive ability. Cadherins 91ycosylated integral membrane proteins that are involved in cell-c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in immuno
                                                                                                                                                                                                                                                                                                                       R86865
                                                                                                                Suzuki S;
WPI; 96-068873/07.
                                                                                                                                                                                                            Homo sapiens. WO9600289-A1.
                                                                                                                                                                                                                                                         Human protocadherin
Protocadherin; pc3;
                                                                                                        N-PSDB; T03572.
                                                                                                                                                                                                                                            catenin; therapy.
                                                                                                                                                                                                                                                                                         R86865;
27-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pemphigus foliaceus antigen-igo constant region;
pemphigus foliaceus; autoantibody; Constant region;
extracellular region; antigen; hinge portion; skin;
extracellular region; antigen protein; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; T66428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dermatitis herpetiformis; fusion protein;
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                                                                                                                                                                                                                                                                                                                                                                                   1 CECNIKVKDVNDNFP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunodiagnosis.
quence 778 AA;
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                                                                                                                                                                                                                                                                                                                       standard;
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12; Conser
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                                                                                                                                                                                                                                                                                                                       Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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                                                                                                                                                                                                                                                           pc3.
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                267
                                                                                                                                                                                                                                                           pc5;
                                                                                                                                                                                                                                                                                                                        787
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 89; DB 21; Le
Pred. No. 1.85e-02;
2; Mismatches 1;
                                                                                                                                                                                                                                                            rat;
                                                                                                                                                                                                                                                           cadherin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 778
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                                                                                                                                                                             FIT Human and rat cadherin polypeptide(s) - mediate cell-cell adhesion
PS Claim 1; Column 69-72; 56pp; English.

CC This sequence represents human cadherin-5. The invention specifically
CC provides details of human cadherin-5, -8, -11, -12 and -13, and rat
CC cadherin-8, -5, -11 and -13. Cadherin are calcium-dependent cell
CC adhesion proteins. They are glycosylated integral membrane proteins
CC that have an N-terminal extracellular domain that determines binding
CC specificity, a hydrophobic membrane spanning region and a C-terminal
CC cytoplasmic domain, which is highly conserved among members of the
CC through eatenins and other cytoskeleton-associated proteins. The
CC cudherins in various cancers. Sequence analysis of the role of
CC cadherins also allows investigation of the structure and function of
CC cadherin. The cadherin proteins may be used to modulate the activity
CC anthodies. These antibodies may also be used to modulate the activity
CC featherin and to determine the tissue specific distribution of cadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
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Best Local Similarity
                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-terminal cytoplasmic domain. The cytoplasmic domain interacts with the cytoplasmic domain is and other cytoskeleton associated proteins. The cytoplasmic domain is not present in all cadherins, but in those which possess it, it is essential for the cadherins adhesive function. The cadherins which do not possess a cytoplasmic domain appear to function via a different method from those with a cytoplasmic domain. These sequences were isolated using primers 1 and 2 (see T03575 and T03576) The proteins may have regulatory functions in the cell, as well as the cell-cell adhesive properties. Antibodies produced against these sequences are useful for modulating the binding activity of these protecacherins, and can be used therapeutically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-APR-1992;
19-APR-1993;
17-APR-1992;
01-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adhesion. Cadherins are composed of an N-terminal extracellular domain which consists of 5 unique subdomains, a membrane spanning domain, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; T85401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suzuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5646250-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cadherin; rat; calcium-dependent cell adhesion protein;
superfamily; cytoskeleton; eatenin; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cadherin-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W25634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W25634 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DOHE-)
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787 AA;
                                                                                                                                       780
                                                                                                                                                                   Each subclass
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US-872643.
US-332638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytoskeleton;
                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 622
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                                                                                50.4%;
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2; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             omains, a membrane spanning domain, and a The cytoplasmic domain interacts with the
                                                                re 57; DB 24; 1
1. No. 4.98e+01;
Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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1.36e+00;
                                                                                                                                                                    unique tissue distribution
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Ca2+ dependent; cell adharan; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-APR-1992;
19-APR-1993;
26-JAN-1994;
                                        Disclosure; Page 16-17; 24pp; Japanese.

The present sequence is used to demonstrate the method of the invention. The specification describes the comparison of DNA base sequences. The method involves 3 steps of: (1) division of a first and second nucleic acid sequence into base groups of three base lengths, and translation into amino acids; (2) all base and amino acid insertions and deletions of the two nucleic acid sequences are observed and the amino acid sequences encoded by these nucleic acid sequences are compared; and (3) adjacent bases and amino acids are compared and step (1) repeated after shifting the translation frame by one base towards the 3' end or shifting the translation frame one base towards the 3' end, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on homologous rat cadherin cDNA.
Antibodies or fragments that specifically bind the human can be used to purify the cadherin, determine its tissue and antagonise its ligand/antiligand binding activities.
Sequence 780 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W13130 standard;
W13130;
                                                                                                                                                                                                      WPI; 99-110965/10.
Comparison of DNA base sequences -
insertions and deletions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Columns 75-78; 59pp; English.
The present sequence is full length human cadherin-5, which
is a Ca2+ dependent cell adhesion protein. The human cadherin
was isolated from a placental cDNA library, using probes based
                                                                                                                                                                                                                                       (HITA ) HITACHI LTD. WPI; 99-110965/10.
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N-PSDB; T61921.
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                                                                                                                                                                                                                                                                    05-MAR-1998;
31-MAR-1997;
                                                                                                                                                                                                                                                                                                                                             DNA sequence
                                                                                                                                                                                                                                                                                                                                                            Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                        W84311;
                                                                                                                                                                                                                                                                                                                                                                                                      T 8
W84311 standard; Protein; 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibodies to cadherin proteins -
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17-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue expression;
             encompassing four bases, and not translating the second or third base. The new method \pm \mathbf{j}_s useful for comparing DNA base sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IKVKDVNDNFP 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ependent; cell adhesion protein; placental; cadherin;
human; antibody; purification; determination;
expression; binding antagonist; calcium ion.
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US-049460.
US-188228.
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JP-079586.
                                                                                                                                                                                                                                                                                                                                             comparison.
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Pred. No. 4.98e+01;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                              exemplify the invention.
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                                                                                                                                                                                                                                                                                                                                                                                      pri plagnosing presence of abnormal epithelial tissue in vitro - respectively. The provided of alpha beta 4 cell surface protein strangle 5; Figure 9; 34pp; English.

Example 5; Figure 9; 34pp; English.

Integrins are heterodimers comrised of alpha and beta subunits, that are non-covalently associated transmembrane glycoproteins. Il alpha chains and 6 beta chains have been recognised in man. Each alpha subunit tends to associate with only one type of beta subunit but there are several exceptions. Integrins mediate (in part) the interaction of cells with the extracellular matrix, forming a link between the extracellular matrix and the cytoskeleton. They may transmit signals from the extracellular to the intracellular environment, affecting cell behaviour. This sequence is the beta4 subunit of an alpha6 beta4 integrin.
                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches
JT 10
R58865;
R58865;
17-APR-1995 (first entry)
Rat-224 cadherin partial sequence.
Cadherin; cell adhesion molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-FEB-1987; US-016552
04-JAN-1989; US-293384
01-OCT-1990; US-591105
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31-JAN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta subunit of integrin cell surface receptor.
Integrin; alpha; beta; subunit; glycoprotein; heterodimer;
transmembrane; extracellular matrix; cell signalling; cytoskeleton;
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19-FEB-1987;
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(QUAR/) QUARANTA V.
                                                                                                                                                                                                 650 ecnfkvkmvde 660
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2 ECNIKVKDVND 12
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Local Similarity 63.6%;
hes 7; Conservative
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94-191533/23.
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617
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491
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Mismatches 5;
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                                                                                                                                                                                                                                                                                                                       DB 10;
6.28e+01;
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Best Local S
Matches 1
                                                                                                                                                                                                  04-JAN-1996.
26-JUN-1995;
27-JUN-1994;
WPI; 96-068873/07.

N-PSDB; T03582.

Polynucleotide(s) encoding human protocadherins pc3 a pc5- involved ip, cell-cell adhesion and regulation a Example 1; Page 40; 146pp; English.

R87102-R87120 represent partial fragments of the rat seguence. The cDNAs encoding these seguences were is
                                                                                                                                                         (DOHE-) DO
Suzuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; Q68957.

Polynuclectide sequences encoding new proto:cadherins - useful for modulating natural binding and regulating activities.

Example: Page 38; 114pp; English.

Two regions of conserved AA sequence, one from the middle of the third cadherin extracellular subdomain (EC-3) and the other from the third cadherin extracellular subdomain (EC-3) and the other from the
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23-DEC-1993; U12588.
29-DEC-1992; US-998003
(DOHE-) DOHENY EYE INS
                                                                                                                                                                                                                                                                 Rattus rattus. W09600289-A1.
                                                                                                                                                                                                                                                                                                         Protocadherin clone RAT-224. Protocadherin; pc3; pc4; pc5; catenin; therapy; clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNAs appear molecules.
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WO9414960-A.
                                                                                                                                                                                                                                                                                                                                                                                                    R87107 standard; Peptide; 43 R87107;
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                                                                                                                                                                             DOHENY EYE
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US-268161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprise a new subclass of cadherin-related
                                                                                                                                                                                INST
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Pred. No. 9.93e+01;
0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                human; rat; cadherin; cell adhesion;
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         it protocadherin isolated after
                                                                   and pc4 and activities
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CC and T03576. The primers were constructed from portions of the amino acid conditions of the third and fourth extracellular domains of published cc cadherin sequences. The full length cDNA sequence encoding rat cc protocadherin pc5 is represented in T03574. The cytoplasmic domain of cc cadherin interacts with the cytoskeleton through cattenins and other cytoskeleton associated proteins. The cytoplasmic domain is not present cd in all cadherins, but in those which possess it, it is essential for the cadherins adhesive function. The cadherins which do not possess a cytoplasmic domain appear to function via a different method from those with a cytoplasmic domain. These protein sequences are involved in cc cell adhesion. These sequences may have regulatory functions in the ccll cell as well as the cell-cell adhesive properties. Antibodies produced cc against these sequences are useful for modulating the binding activity of these protocadherins, and can be used therapeutically.
PT Helicobacter pylori nucleic acid sequences and encoded PT polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection PS Claims 14,94; Page 677-678; 1145pp; English.

CC This sequence is a H. pylori secreted protein.

CC This sequence is a H. pylori secreted protein.

CC This sequence is a H. pylori polypeptide binding compounds, compounds, compounds in the protein may be used in a vaccine to prevent or treat H. pylori CC useful as potential H. pylori polypeptide binding compounds, com
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27-MAR-1997; U05223.
06-DEC-1996; US-761318.
29-MAR-1996; US-625811.
02-APR-1996; US-758731.
25-OCT-1996; US-736905.
28-OCT-1996; US-738859.
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H. pylori ORF 06apl1119_16594193_fl_9 secreted protein.

Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacteria; life cycle; and the cycle; chronic destriction; disease; chronic gastritis; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori. W09737044-A1.
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Alm RA, Smith D;
WPI; 97-503122/46.
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Similarity 66.7%;
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RESULT
ID WI
AC WI
DT 14
DE HI
KW C2
KW D1

JT 14 W13139 standard; Protein; W13139;

AA

14-MAY-1997 (first entry)
Human cadherin-Lantigenic epitope (residues 242-252).
Ca2+ dependent; cell adhesion protein; cadherin; human; antibody; purification; determination; epitope; tissue expression; binding antagonist; calcium ion; antigen.

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1 CECNIKVKDV 10

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                                                                                                                                                           Pri Helicobacter pylori nucleic acid sequences and encoded pri Helicobacter pylori nucleic acid sequences to treat or prevent H. pylori priestion and for diagnosis of H. pylori infection for diagnosis of H. pylori infection for diagnosis of H. pylori infection for treat H. pylori protein may be used in a vaccine to prevent or treat H. pylori protein may be used in a vaccine to prevent or treat H. pylori confection for to identify H. pylori polypeptide binding compounds, for useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of CC acid sequences complementary to the DNA act as antisense sequences and CC can be used to prevent the translation of H. pylori infection. Nucleic can be used to prevent the translation of H. pylori mRNA. Antibodies CC against the protein can be used in immunoassays to evaluate the abundance CC and distribution of H. pylori-specific antigens. The genomic sequence of CC H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF cere analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR constrained the sequences of interest, particular regions can be isolated from H. pylori by PCR constrained the sequences of interest, particular regions can be isolated from H. pylori by PCR constrained the sequences of interest, particular regions can be isolated from H. pylori by PCR constrained the sequences of interest, particular regions can be isolated from H. pylori by PCR constrained the sequences of interest particular regions can be solated from H. pylori by PCR constrained 
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06-DEC-1996; US-761318.

29-MAR-1996; US-628811.

02-APR-1996; US-758731.

25-OCT-1996; US-738905.

28-OCT-1996; US-738859.
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WO9737044-A1.
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                                                                                                                              Sequence
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47 cncnikipsi 56
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ORF 11ge10309orf7 protein.
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llarity 50.0%;
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                                     Score 53; DB 29;
Pred. No. 1.25e+02;
3; Mismatches 2
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(DOHE-) DOHENY EYE INST. Suzuki, 97-108328/10. Antibodies to cadherin proteins - useful as cadherin antagonists,

Homo sapiens. US5597725-A. 28-JAN-1997. 17-APR-1992; 872643. 17-APR-1992; US-872643. 19-APR-1993; US-972643. 26-JAN-1994; US-188228.

S B

1 vtlqdindnfp 11 : : |:|||| 5 IKVKDVNDNFP 15 Query Match 46.0%; Best Local Similarity 54.5%; Matches 6; Conservative

Score 52; DB 21; Pred. No. 1.56e+02; 3; Mismatches 2

Length 11; 2; Indels

0;

Gaps

0

Claim 5; Column 112; 59pp; English.

The present sequence is an antigenic epitope from human cadherin-5, which is a Ca2+ dependent cell adhesion protein. Antibodies or fragments that specifically bind the epitope can be used to purify the cadherin, determine its tissue expression and antagonise its ligand/antiligand binding activities.

Sequence 11 AA;

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                                                                                                                           petection of t(1,19) break-point-associated genes E2A and pr1 in chromosomal translocation, and prods. useful in diagnosis and therapy of human neoplasm, esp. acute lymphoblastic leukaemia pisclosure; Fig 1D; 104pp; English.

The E2A gene (see Q13659), encoding immunoglobulin enhancer-binding factors E12 and E47 (see Q13670 and Q13671), is localised to the breakpoint of a consistently recurring chromosomal translocation t(1:19) chromosomal translocations. The translocation results in synthesis of a fusion mRNA (see Q13672 for fusion cDNA) that crosses the breakpoint between chromosome 1 and 19.

The CDNAs of E12 and E47 encode nearly identical proteins contg. a region that appears to represent a novel helix-loop-helix DNA-binding and dimerisation motif. The motif shares significant homology with domains in several proteins involved in the control of differentiation and proliferation in various cellular lineages. See also Q1369-75.
                                                               Query Match
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Matches
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02-FEB-1991; U01168.
23-FEB-1990; US-484063.
23-FEB-1990; US-484063.
(STRD ) LELAND STANFORD JR UNIV.
(WHIT-) WHITEHEAD INST BIOMED RE.
(CLEARY ML, Mellentin JD, Baltimore D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E47 cDNA prod. (pE47P).
Immunoglobulin; enhancer-binding factor; E12; E47; E2A;
chromosomal translocation; leukemia; fusion protein.
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R13947 standard; Protein; 132 AA.
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IKVKDVNDNF 14
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larity 40.0%;
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Search completed: Fri Jun 11 17:44:58 1999 Job time: 111 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:38:59 1999; MasPar time 4.29 Seconds 140.011 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-991-628-5 (1-15) from US08991628.pep 113 1 CECNIKVKDVNDNFP 15

Scoring table: PAM 150 Gap 15

Searched: 122810 segs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

Mean 25.852;

Variance 36.674; scale 0.705

pir60 1:pir1 2:pir2 3:pir3 4:pir4

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

Query Match Best Local Sim Matches 15;	SUMMARY	910-938 937-966 110,180,545	496-598 616-639 640-999	52-157 160-267 270-383 390-495	24-49 50-999 50-615	FEATURE 1-23	#map_position CLASSIFICATION KEYWORDS	#gene #gene ##cross-re	##molecule_type mR ##residues 1.1 ##cross-references	#cross-referer	#journal #title	ACCESSIONS REFERENCE #authors	RESULT 1 ENTRY TITLE TALE ALTERNATE_NAMES ORGANISM DATE
1 100.0%; Score 113; DB 1; Length 999; Similarity 100.0%; Pred. No. 3.28e-12; 15; Conservative 0; Mismatches 0; Indels 0; Gaps	#length 999 #molecular-weight 107502 #checksum 8311	#domain desmoglein repeat #label DG1\ #domain desmoglein repeat #label DG2\ #binding_site carbohydrate (Asn) (covalent) #status	cadherin repeat homology transmembrane #status pre intracellular #status pre	cadherin repeat nomology #label cadherin repeat homology #label cadherin repeat homology #label cadherin repeat homology #label	propeptide #status predicted #lit desmoglein homolog #status pred extracellular #status predicted	uence #status predicted #label	#superfamily cadherin; cadherin repeat homology calcium binding; cell adhesion; duplication; glycoprotein; transmembrane protein	н,	##molecule_type mRNA 1-999 ##label AMA ##cross-references GB:M76482; NID:g190751; PID:g190752		Cell (1991) 67:809-877 Autoantibodies against a novel epithelial cadherin in		
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CLASSIFICATION
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ENTRY
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*cross-references MUID:92037656
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##cross-references GB:S64268; GB:S64270
A37785
                                                                                                   ##cross-references GB:X57784

##note this sequence has been revised in references A38872 and
S38721
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##cross-references EMBL:X58466; NID:g306; PID:g307
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Complete sequence of the desmoglein precursor and evidence for the existence of different desmoglein genes expressed in cell type-specific patterns.
                                                                                                                                                                                                                                                    Koch, P.J.; Walsh, M.J.; Schmelz, M.; Goldschmidt, M.D.; Zimbelmann, R.; Franke, W.W.
Eur. J. Cell Biol. (1990) 53:1-12
Identification of desmoglein, a constitutive desmosomal glycoprotein, as a member of the cadherin family of cell adhesion molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, February 1991 838721
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Franke, W.W.
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                  #superfamily cadherin; cadherin
calcium binding; cell adhesion;
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         repeat homology duplication; glycoprotein;
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##residues 24-1049 ##label WHE
##cross-references GB:X56654
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Similarity 80.0%;
12; Conservative
                                                                                                                                                                 Wagner, R.M.; Green, K.J.
J. Cell Sci. (1991) 99:809-821
Structural analysis and expression of human
cadherin-like component of the desmosome.
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desmosomal glycoprotein I
#formal_name Homo sapiens #common_name man
30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
26-Feb-1998
Wheeler, G.N.; Buxton, R.S.; Parker, A.E.; Rees, D.A.; King, I.A.; Magee, A.I. Biochem. Soc. Trans. (1991) 19:1060-1064 Desmosomal glycoproteins I; II and III: no
                                                                                                                                                                                                                                                     Nilles, L.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wheeler, G.N.; Parker, A.E.; Thomas, C.L.; Ataliotis, Poynter, D.; Arnemann, J.; Rutman, A.J.; Pidsley, S. Watt, F.M.; Rees, D.A.; Buxton, R.S.; Magee, A.T.; Proc. Natl. Acad. Sci. U.S.A. (1991) 88:4796-4800
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#domain transmembrane #status predicted #label TMM\
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#domain desmoglein repeat #label DG3\
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#map_position 18q12.1-18q12.2
CLASSIFICATION #superfamily cadherin; cadherin
KEYWORDS calcium hinding.
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#cross-references MUID:92175187
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#*residues 1-171 ##label MCL
##cross·references EMBL:Z67999; NID:g1067216; PID:g1067219
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##residues 1-55 ##label WH3
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                                      CQCSVKIRSVLTDF 89
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   CECNIKVKDVNDNF
                                                                          Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein SPAC21E11.03c - fission yeast (Schizosaccharomyces pombe)
#formal_name Schizosaccharomyces pombe
16-May-1996 #sequence_revision 13-Mar-1997 #text_change
31-Oct-1997
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#length 171
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                                                                      58.4%;
larity 35.7%;
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#binding_site carbohydrate (
    predicted
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#domain desmoglein repeat #label DG2\
#domain desmoglein repeat #label DG3\
#domain desmoglein repeat #label DG4\
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#domain propeptide #status predicted #label PRO\
#product desmoglein #status predicted #label MAT\
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#domain cadherin repeat homology #label CR1\
#domain cadherin repeat homology #label CR2\
#domain cadherin repeat homology #label CR3\
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domain cadherin repeat homology #label
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                                                                                                                                              fos/jun DNA-binding domain homology #label
#molecular-weight 19348 #checksum 9337
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Pred. No. 1.
2; Mismatc
                                                                        Score 66; DB 2; I
Pred. No. 9.35e-02;
6; Mismatches 3
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1.28e-06;
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Best Local Similarity 53.8%;
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135-189
203-258
272-324
                                                                                                                                    #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #title Complete genome sequence of the methanogenic archaeon,
Methanococcus jannaschii.
#cross-references MUID:96337999
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                                                                                              #cross-references MUID:92108053
                                                                                                                                                                                          #authors
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##residues 1-394 ##label BUL
##cross-references GB:U67560; GB:L77117; NID:g1591813; PID:g1591821;
##cross-references GB:MJ1193; PID:g1511192
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##molecule_type_mRNA
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                                                                                                                                                                                                                                                                 IJBODD #type fragment desmocollin 2b precursor - bovine (fragment) epithelial type 2 desmocollin subform II #formal_name Bos primigenius taurus #common_name cattle #formal_name #formal_name fragment formal_name fragment formal_name fragment formal_name fragment formal_name fragment formal_name fragment formal_name fragment formal.
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13-Sep-1996 #sequence_revision 13
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                                                                                                                                                                                                                                                 05-Sep-1997
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translation not shown
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ferredoxin 2[4Fe-4S] homology #label
ferredoxin 2[4Fe-4S] homology #label
ferredoxin 2[4Fe-4S] homology #label
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ferredoxin 2[4Fe-4S] homology
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Pred. No. 3.57e-01
3; Mismatches
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                                                                                                                                    patterns
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FER2\
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FEATURE 1-89

GENETICS

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##experimental_source muzzle
##note sequence extracted from NCBI backbone
##note 264-Gln and 333-Gln were also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##residues
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Local Similarity 61.5%;
hes 8; Conservative
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epithelial type 2 desmocollin subform I
#formal_name Bos primigenius taurus #common_name cattle
30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
05-Sep-1997
                                                                                                                                                                                                                                                                                                                           *superfamily cadherin; cadherin repeat homology alternative splicing; calcium binding; cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. (1992) 89:353-357
Complexity and expression patterns of the desmosomal
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alternative splicing; calcium binding; cell adhesion;
duplication; glycoprotein; transmembrane protein
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R.; Franke, W.W.
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                                                                                                                                                                                                                                                                                                            duplication; glycoprotein; phosphoprotein; transmembrane
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#domain intracellular #status predicted #label INT\
#binding_site carbohydrate (Asn) (covalent) #status
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#product desmocollin 2b #status predicted #label MAT\
#domain extracellular #status predicted #label EXT\
#domain cadherin repeat homology #label CR1\
#domain cadherin repeat homology #label CR2\
#domain cadherin repeat homology #label CR3\
#domain cadherin repeat homology #label CR4\
#domain cadherin repeat homology #label CR4\
#domain cadherin repeat homology #label CR5\
                       #binding_site carbohydrate (Asn)
predicted\
                                                                                                #domain propeptide #status predicted #label PRO\
#product desmocollin 2a #status predicted #label MA'
#domain extracellular #status predicted #label EXT\
#domain cadherin repeat homology #label CR1\
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#domain cadherin repeat homology #label CR3\
#domain cadherin repeat homology #label CR3\
#domain cadherin repeat homology #label CR4\
#domain cadherin repeat homology #label CR4\
binding_site phosphate (Ser) (covalent) #status
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Pred. No. 1.31e+00;
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275 ECPIATKTINEEYP 288
                                                                                                                                                                                                       ##cross-references
                                                                                                                                                                                                                        ##residues
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RESULT

ORGANISM

å В SUMMARY

FEATURE 1-89

KEYWORDS

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Query Match 53.1%;
Best Local Similarity 69.2%;
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Best Local Similarity 61.5%;
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                                                                                                                                                         ##molecule_type DNA ##residner
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#*residues 1-896 #*label YUE
##cross-references GB:L33774; NID:g914820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 CNIKVKDVNDNFP 15
   Similarity 42.9% 6; Conservative
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J. Cell Sci. (1995) 108:2163-2173
Characterisation of a desmocollin isoform (bovine DSC3)
exclusively expressed in lower layers of stratified
                                                                                                                                                                                                                                                                                                           hypothetical protein SPAC4G8.07c - fission (Schizosaccharomyces pombe)
#formal_name Schizosaccharomyces pombe
16-May-1996 #sequence_revision 13-Mar-1997
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19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change
13-Mar-1998
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                                                                 125/1; 158/2; 437/3; 520/3
#length 527 #molecular-weight 59613
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es EMBL:Z56276; NID:g1022345;
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1 863 #checksum 1299
                   51.3%;
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the EMBL Data
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Pred. No. 1.31e+00;
1; Mismatches 3
Score 58; DB 2; 1
Pred. No. 3.06e+00,
4; Mismatches 4
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Pred. No. 1.31e+00;
3; Mismatches 2
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M.; Nakaseko, Y.; Yanagida, M.
#journal EMBO J. (1994) 13:4938-4952
#title Fission yeast cut3 and cut14, members of a ubiquitous protein family, are required for chromosome condensation and segregation in mitosis.

#cross-references_MUID:95045386
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##restidues 1-832 ##label BOE
##cooss-references EMBL:X83228; NID:g854174; PID:g854175
#ETCATION #superfamily cadherin repeat homology
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                                                                                                                                                200 CDVEITFKEVNSDF 213
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##cross-references EMBL:D30788; NID:g577659; PID:d1007025; PID:g603501
#Y #length 1324 #molecular-weight 150593 #checksum 3330
                                                                                                                                                                                                                                                                                                                              ##molecule_type DNA
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Local Similarity 42.9%;
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Local Similarity 64.3%;
nes 9; Conservative
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2 ECNIKVKDVNDNFP 15
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cut3 protein - fission yeast (Schizosaccharomyces pombe)
#formal_name Schizosaccharomyces pombe
15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change
09-Sep-1997
DNA replication protein DnaC - #formal_name Aquifex aeolicus 08-May-1998 #sequence_revision
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                                                        #type complete
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Pred. No. 3.06e+00;
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Pred. No. 3.06e+00;
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     08-May-1998 #text_change
                                     Aquifex aeolicus
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Best Local Similarity 63.6%;
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#accession E70378
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##cross-references GB:AE000713; NID:g2983424;
##experimental_source strain VF5
                 ##molecule_type protein
48-60,'x',62,'x',54;108-115,'x',118-123;237-238,'x',240,
##residues
'X',242-252,'x',254-256;263-275,'X',277-283,'x',285;
'X',425-429 ##label LAM
##experimental_source cultured endothelial cells
##experimental_source cultured endothelial cells
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!NCE $24305
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Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.;
Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short,
J.M.; Olson, G.J.; Swanson, R.V.
Nature (1998) 392:353-358
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Cell Regul. (1991) 2:261-270
Diversity of the cadherin family: evidence for eight new
cadherins in nervous tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Breviario, F.; Caveda, L.; Corada, M.; Martin-Padura, Golay, J.; Introna, M.; Lampugnani, M.G.; Dejana, E. submitted to the EMBL Data Library, June 1994 Molecular and functional properties of VE-cadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cadherin 5 precursor - human 784 antigen; cadherin, endothelial-specific; VE-cadherin #formal_name Homo sapiens #common_name man 30-Jun-1993 #sequence_revision 13-Sep-1996 #text_change 05-Sep-1997 1011
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translation not shown
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Best Local Similarity 81.8%;
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Abu-Alfa, A.; Soleimani, M.; Aronson, P.S.
#journal J. Biol. Chem. (1995) 270:17594-17601
#title Isolation and cDNA cloning of Ksp-cadherin, a novel
kidney-specific member of the cadherin multigene
#cross-references MUID:95340560
#accession 146536
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523,535
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                                                                                                                                                                                                                                                                             ##residues 1.829 ##label THO
##cross-references EMBL:U28945; NID:g902885;
# #length 829 #molecular-weight 888
                                                                                                                                                                                                                                                                                                                                                ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                           ##status
                                                                                                                                                                                                                     Y Match 50.4%; Local Similarity 53.3%;
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                                                                                                               CECNIKVKDVNDNFP 15
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NCBIP:113051, NCBIP:113054)
Cadherins mediate calcium-dependent intercellular adhesion, and are thought to be involved in the sorting of different cell types
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calcium binding; cell adhesion; duplication; glycoprotein;
IJHUDB #type complete desmocollin 3b precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change
14-Feb-1997
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#formal_name
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#region serine-rich\
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#domain cadherin repeat homology #label CR2\
#domain cadherin repeat homology #label CR3\
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#domain transmembrane #status predicted #lab
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n - rabbit
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Pred. No. 4.65e+00
2; Mismatches
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Pred. No. 4.

    human

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4.65e+00;
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88827 #checksum
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Search completed: Fri Jun 11 Job time: 87 secs.

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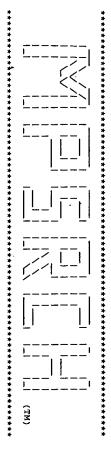
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ACCESSIONS
REFERENCE
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#map_position 18q12.1-18q12.1

CLASSIFICATION #superfamily cadherin; cadherin repeat homology

Alternative splicing; calcium binding; cell adhesion;

KEYWORDS duplication; glycoprotein; phosphoprotein; transmembrane
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                                                                                                      Query Match
Best Local
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#title Desmosomal glycoproteins II and III. Cadherin-
molecules generated by alternative splicing.
#cross-references MUID:91244819
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136-695
                                          341 CIINIDDVNDHLP 353
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##note it is uncertain whether Met-1 is the initiator
whether translation is initiated upstream to
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##residues 1-847 ##label PAR
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  CNIKVKDVNDNEP
                                                                                h 50.4%;
Similarity 53.8%;
7; Conservative
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K.J.; King, I.A.; Koch, P.J.; Magee, A.
Stanley, J.R.; Steinberg, M.S.
J. Cell Biol. (1993) 121:481-483
Nomenclature of the desmosomal cadherins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  desmosomal glycoprotein III
#formal_name Homo sapiens #common_name man
30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDB:DSC3; DSC2;
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#domain intracellular #status predicted #label INT\
#binding_site carbohydrate (Asn) (covalent) #status
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#domain propeptide #status predicted #label PRO\
#product desmocollin 3b #status predicted #label MAT\
#domain extracellular #status predicted #label EXT\
#domain cadherin repeat homology #label CR1\
#domain cadherin repeat homology #label CR3\
#domain cadherin repeat homology #label CR5\
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A.I.; Rees,
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:36:11 1999; MasPar time 2.45 Seconds 172.800 Million cell updates/sec

Tabular output not generated.

Title: Description: Perfect Score: >US-08-991-628-5 (1-15) from US08991628.pep 113

Sequence: 1 CECNIKVKDVNDNFP 15

Scoring table: РАМ 150 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Mean 26.658;

Variance 31.710;

scale 0.841

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22222987 3322222987 332222987	Result
113 5544 5544 5544 5544 5544 5544 5544 5	Score
100.00 78.00 78.00 53.1.4 44.00 50.4.4 47.886.064.4 47.886.064.6 90.64.6	Query Match
999 1049 1049 171 863 896 709 709 780 902 527 1324 783 783 784 1324 1324 1324 1324 1324 1324 1324 132	Length
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ALIGNMENTS

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752; 3. CADHERIN; herin; 4.	SWISS-PROT entry is copyrige een the Swiss Institute of European Bioinformatics Institution on profit institution fied and this statement is notices agree the requires a license agree end an email to license@isbend an email to license@isbend.	DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN LINE REFERS SEED	UENCE FROM N.A. LINE; 92069753. GAI M., KLAUS-KOVTUN V., STANLEY J.R.; toantibodies against a novel epithelial cadherin in garis, a disease of cell adhesion."; £ 67:869-877(1991). FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUN FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUN INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND FILAMENTS MEDIATING CELL-CELL ADHESION. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL, OES CARCINOMAS.	LT 1 10533_HUMAN STANDARD; PRT; 999 AA. 193926; 101-OCT-1993 (REL. 27, CREATED) 101-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE) 101-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) 101-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) 101-NOV-1997 (REL. 37, LAST ANNOTATION UPDATE) 101-NOV-1997 (REL. 37, LAST ANNOTATION UPDATE) 10253. 1033. 1034. 1035. 1036

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01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
01-NOV-1993 (REL. 35, LAST ANNOTATION UPDATE)
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SOS TAUGUS (BOVINE).
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DOMAIN
adhesion molecules.";
BIOCHEM. BIOPHYS. RES. COMMUN. 173:1224-1230(1990).
-!- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS FILAMENTS MEDIATING CELL-CELL ADHESION.
                                                                                                                                                                                  glycoprotein, as a
molecules.";
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MEDLINE; 91168965.
KOCH P.J., WALSH M.J., SCHMEL
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-MUZZLE EPITHELIUM;
KOCH P.J., GOLDSCHMIDT M.D.,
SUBMITTED (MAR-1991) TO EMBL
                                              SEQUENCE OF 44-493 FROM N.A.
MEDLINE, 91097553.
GOODWIN L., HILL J.E., RAYNOR K., RASZI
"Desmoglein shows extensive homology to
                                                                                             "Complete amino acid sequence of the polypeptide and identification of a seur. J. CELL BIOL. 55:200-208(1991).
                                                                                                                           FRANKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                      REVISIONS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADHESION;
                                                                                                                           W. W. ;
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                                                                                                                                                                         CELL BIOL.
                                                                                                                                            92037656
                                                                                                                                                     AND SEQUENCE OF
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                                                                                                                                   GOLDSCHMIDT
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                                                                                                                                   M.D.,
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                                                                                                                                                                                                                       SCHMELZ M.,
                                                                                                                                                                                                                                                                     M.D., ZIMBELMANN R., FRANKE W.W.; EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                          lein, a of the
                                                                                                                                                      101-123.
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Pred. No. 6.78e-15;
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DESMOGLEIN
DESMOGLEIN
POTENTIAL.
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CADHERIN
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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                                                                                                      type
                                               MANABE M.
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                    JUNCTIONS
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                                              family o
          INTERMEDIATE
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of cell
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SIGNAL 1
PROPER 24
CHAIN 50
DOMAIN 50
TRANSMEM 549
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01-OCT-1993
01-OCT-1993
01-NOV-1997
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CONFLICT
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                                                                                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
PRIMATES; CATARRHINI; HOMINID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X58466; G307; -. EMBL; X57784; G436062; -. EMBL; M58165; G552318; -.
ARNEMANN J., RUTMAN A.J., BUXTON R.S., MAGEE A.I.;
                             TISSUE-KERATINOCYTES;
MEDLINE; 91271279,
WHEELER G.N., PARKER A.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP;
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PROSITE; PS00232; CADHERIN;
                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                            DESMOGLEIN 1
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1 CECNIKVKDVNDNFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P09803;
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12; Conser
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larity 80.0%;
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27, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE
35, LAST AND UPDATE
35, LAST
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                                                                                                                        HOMINIDAE;
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2; 1
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Pred. No. 2.56e-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is produced through a collaboration and the EMBL outstation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REF. 4).
84 CRC32;
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                WATT F.M., REES
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                                   POYNTER D.,
                  D.A.,
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PIR; S16906; IJHUG1.
MIM; 125670; -.
PROSITE; PS00232; CADHERIN; 2
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CARBOHYD
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                                             PCR1_SCHPO STANDARD; PRT; 171 AA.

009926;
01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
TRANSCRIPTION FACTOR PCR1 (TRANSCRIPTION FACTOR PCR1 (TRANSCRIPTION FACTOR PCR1 OR MTS2 OR SPAC21E11.03C.
SCHIZGSACCHAROMYCES POMBE (FISSION YEAST).
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DOMAIN
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CELL ADHESION; SIGNAL;
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                          EUKARYOTA; FUNGI; ASCOMYCOTA; SCHIZOSACCHAROMYCETALES; SCHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
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                                                                                                                                                                                   1 CECNIKVKDVNDNFP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CO. NATL. ACAD. SCI. U.S.A. 88:4796-4800(1991).

FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS.

INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIFILAMENTS MEDIATING CELL-CELL ADHESION.

FILAMENTS MEDIATING CELL-CELL ADHESION.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSILAND OESOPHAGUS.

DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
SIMILARITY: BELONGS
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                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-profit institutions as long as its content is and this statement is not removed. Usage by and for requires a license agreement (See http://www.isb-sib-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     email to license@isb-sib.ch).
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llarity 80.0%;
Conservative
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545
570
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270
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                                                                                                                                                                                                                                                                                113715
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                          COTA; ARCHIASCOMYCETES; SCHIZOSACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                        DESMOGLEIN REPEAT 1
DESMOGLEIN REPEAT 2
DESMOGLEIN REPEAT 3
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2; N
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                                                                                                                                                                                                                                              Score 89; DB 1; 1
Pred. No. 2.56e-08
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EXTRACELLULAR (POTENTIAL).
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15-JUL-1998
DESMOCOLLIN
(FRAGMENT).
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P33545;
01-FEB-1994
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DNA_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 96140438.
WATANABE Y., YAMAMOTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCLEAN J., HARRIS D., SUBMITTED (NOV-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KON N., KRAWCHUK M.D
SUBMITTED (FEB-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Schizosaccharomyces pombe pcrl+ encodes a CREB/ATF protein involved in regulation of gene expression for sexual development."; MOL. CELL. BIOL. 16:704-711(1996).
                                                                                            DSC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00170; bZIP; 1. HSSP; P05412; 1FOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D63667; G1199496; -. EMBL; U87870; G1839252; -. EMBL; Z67999; E1168681; -. EMBL; Z67999; E1768681; -. PROSITE; PS00036; BZIP_BASIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SUBUNIT: HETERODIMER OF PCR1/MTS2 AND ATF1/MTS1.
-i- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-i- SIMILARITY: TO OTHER BZIP PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity.";
GENES DEV. 8:1693-1702(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recombination hot spot:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 95047325.
WAHLS W.P., SMITH G.R.;
"A heteromeric protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION
                                               BOS TAURUS EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ÷
ARTIODACTYLA; RUMINANTIA; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSCRIPTION REGULATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       76 CQCSVKIRSVLTDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENT. BINDS
                                                                                                                                                                                                                                                                                                                                               CECNIKVKDVNDNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRAWCHUK M.D.,
                (BOVINE).
METĀŽOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
METĀŽOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
METĀŽOA; CHORDATA; BOVOIDĒA; BOVIDĀE; BOVINĀE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 AA;
                                                                                                                                        (REL.
(REL.
(REL.
2A/2B
                                                                                                                                                                                                                                                                                                                                                                                                                                   58.4%;
larity 35.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
42
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                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                      28, CARATED)
28, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
PRECURSOR (EPITHELIAL TYPE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32
66
19348
                                                                                                                                                                                                                                                                                                                                                                                         89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ., WARREN B.G., SMITH TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BARRELL B.G., RAJANDREAM M.A., TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               that binds to correlation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVATOR; DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 66; DB 1; Le
Pred. No. 1.22e-02;
6; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASIC MOTIF.
                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0D025155 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF GENE
                                                                                                                                                                                                                                                          863
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                                                                                                                                                                                                                                                          A
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DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RECOMBINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homologous
and hot spot
                                                                                                                                           DESMOCOLLIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WALSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R SEXUAL
HOT SPOT
                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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VARIANT
VARSPLIC
                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
CARBOHYD
DSC3_BOVIN STANDARD;
Q28060; Q28061; Q28176;
Q1-NOV-1997 (REL. 35, CR
                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
DOMAIN
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unis SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complexity and expression patterns of the desmosomal cadherins.";
PROC. NATL. ACAD. SCI. U.S.A. 89:353-357(1992).

-:- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO EPIDERMAL CELL POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- TISSUE SPECIFICITY: OESOPHAGUS AND RUMEN. WEAKLY IN EPITHELIA AND
                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                  PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00028; cadherin; 4. HSSP; P09803; ISUH. CELL ADHESION; GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR: A41799; IJBODC.
PIR: B41799; IJBODD.
PROSITE; PS00232; CADHERIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-MUZZLE EPITHELIUM
MEDLINE; 92108053.
                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRANKE W.W.;
                                                                                                    295 CIINIEDVNDNLP
                                                                                                                                        Local
                                                                           3 CNIKVKDVNDNEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARDIAC MUSCLE.

DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE SPLICING OF THE SAME GENE. SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS TO THE DESMOSOMAL SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M81190; G163758; -. M81190; G163759; -.
                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOLDSCHMIDT M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          SPLICING;
                                                                                                                            Conservative
                                                                                                                                                                               B
                                                                            15
                                                                                                   307
                                                                                                                                        53.1%;
  CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOSKELETON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : FORMS
                                                                                                                                                                               ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
                                                                                                                          Score 60; DB 1; I
Pred. No. 2.61e-01;
3; Mismatches
                                                                                                                                                                                                                                                                                             CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
                                                                                                                                                                        K -> Q.

R -> Q.

K -> Q.

KYQQCDODITH -> ESIRGHTLVKN (IN FORM MISSING (IN FORM 2B).

; 2173F06E CRC32;
                                                                                                                                                                                                                   POTENTIAL.
K -> Q.
R -> Q.
                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEMBRANE; REPEAT; ELETON; CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIMBELMANN R.,
                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC CADHERIN 1.
                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                      DESMOCOLLIN 2A/2B.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAME GENE.
                            896
                          A
                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HERE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TROYANOVSKY
                                                                                                                                                    Length 863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND
                                                                                                                           Indels
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                                                                                                                           Gaps
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VARSPLIC
VARSPLIC
CARBOHYD
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE; 95403557.

YUE K.K.M., HOLTON J.L., CLARKE J.P., HYAM J.L.M., HASHIMOTO T.,

CHIDGEY M.A.J., GARROD D.R.;

"Characterisation of a desmocollin isoform (bovine DSC3) exclusively
expressed in lower layers of stratified epithelia.";

J. CELL SCI. 108:2163-2173(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BOS TAURUS (BOVINE).
BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTTODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; BOVINAE;
                                                                                       REPEAT
                                                                                                  DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                               EMBL; L33774; G914821; -. EMBL; L33774; G914822; -. EMBL; X75783; G433870; -.
                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).

-!- ALTERNATIVE PRODUCTS: FORMS 3A AND 3B ARE PRODUCED BY A SPLICING OF THE SAME GENE.
-!- SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESMOCOLLIN DSC3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                   PFAM; PF00028; cadherin; HSSP; P09803; 1SUH.
                                                                                                                                                                                                                                                                                                                                                                                                         -!- DOMAIN: CALCIUM MAY BE BOUND BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GARROD
                                                                     DOMAIN
                                                                               REPEAT
                                                                                                                               TRANSMEM
                                                                                                                                                             PROPEP
                                                                                                                                                                                                                       PROSITE; PS00232; CADHERIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 94308280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-EPIDERMIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 686-814
                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGAN P.K., YUE K.K.M., CHIDGEY M.A.J., HOLTON J.L., WILKINSON R.W.,
                                                                                                                                                                                                                                                                                                                                                        DESMOSOMAL SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REL.
                                                                                                                      1
27
135
135
691
712
                                                                                                                                                                                 SPLICING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3A/3B
                                                                                                                                                                                           GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRECURSOR.
 FROM N.A.
                                                                                                                                                                               ROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL; CYTOSKELETON; CALCIUM-BINDING.
CADHERIN 5
KLHLCNQD -:
MISSING (II
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
VI -> EF ()
                                                                                      CADHERIN 2.
CADHERIN 3.
                                                                                                          CYTOPLASMIC (POTENTIAL). CADHERIN 1.
                                                                              CADHERIN
                                                                                                                               POTENTIAL
                                                                                                                                         EXTRACELLULAR
                                                                                                                                                             POTENTIAL
                                                                                                                                                   DESMOCOLLIN 3A/3B
                                                                                                                                                                                                                                                                                                                                                                                                         THE CADHERIN-LIKE
                                                 (IN
 (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                    3B ARE PRODUCED BY ALTERNATIVE
                                                ESIRGHTG
FORM 3B).
                                                                                                                                         (POTENTIAL).
2)
                                                         ΩÏ
                                                           FORM 3B).
                                                                                                                                                                                                                                                                                                               restrictions on
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                                                                                                                                                                                                                                                                                                                            collaboration
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RESULT ACCOUNTS OF THE COLOR OF
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Best Local s
Matches
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Matches
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                                                                                                                                                                                     OBP_HSV6Z STANI
P52452;
01-OCT-1996 (REL. 34
01-OCT-1996 (REL. 34
01-NOV-1997 (REL. 31
REPLICATION ORIGIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                                             U73 OR CH6R.
U73 OR CH6R.
HERPES SIMPLEX VIRUS (TYPE 6 /
VIRUSES; DSDNA VIRUSES, NO RNA
VIRUSES; DSDNA PROSECLOVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U12964; WOZAFE, CE01258.
WORMPEP; F26F4.10; CE01258.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
PFAM; PF00750; tRNA-Synt_Id; 1.
PFAM; PF00750; tRNA-SYNTHETASE; PROTEIN BIOSYNTHESIS;
AMINOACYL-TRNA SYNTHETASE; PROTEIN BIOSYNTHESIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBMITTED (NOV-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.

-I- CATALYTIC ACTIVITY: ATP + L-ARGININE + TRNA(ARG) = AMP +
PYROPHOSPHATE + L-ARGINYL-TRNA(ARG).

-I- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).

-I- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYR_CAEEL Q19825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (REL. 35, PROBABLE ARGINYL-TRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FULTON L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RHABDITINA;
SEQUENCE FROM N.A. MEDLINE; 96195263. LINDQUESTER G.J.,
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Similarity 54.5%;
6; Conservative
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709 AA;
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. 34, LAST SEQU
. 35, LAST ANNO
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  INOUE N.,
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OIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.1%;
69.2%;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
SYNTHETASE (EC 6.1.1.19)
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PROTEIN (OBP).
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Pred.
1; M
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Pred. No. 4.27e-01;
4; Mismatches 1
  ALLEN R.D.,
                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                               STRAIN Z29)
STAGE; HERP
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d. No. 2.61e-01;
Mismatches 3;
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                                                                                                                                                                                                                                                                                                          780
                                                                                                                    HERPESVIRIDAE;
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ong as its content is in no
  CASTELLI J.W.
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Best Local s
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       OBP_HSV6U
P52378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Restriction endonuclease mapping and molecular cloning of therpesvirus 6 variant B strain 229 genome.";
ARCH. VIROL. 141:367-379(1996).
-i- EUNCTION: PROBABLY INVOLVED IN DNA REPLICATION. BINDS THE
OF REPLICATION (ORI) (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1
                                                                                                                            MEDLINE; 95266321.
GOMPELS U.A., NICHOLAS J., LAWRENCE G., JG
MARTIN M.E., EFSTATHIOU S., CRAXTON M., M
"The DNA sequence of human herpesvirus-6:
and genome evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA REPLICATION; DNA-BINDING; ATP-BINDING.
NP_BIND 52 59 ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                             This
                                                                                                                                                                                     conserved herpesvirus glycoprotein
                                                                                                                                                                                                                                                                                                                                                          BETAHERPESVIRINAE;
                                                                                                                                                                                                                                                                                                                                                                     U73 OR 19R OR HDRFO.
HERPES SIMPLEX VIRUS (TYPE 6 /
VIRUSES; DSDNA VIRUSES, NO RNA
                                                                                                                                                                                                  MEDLINE; 95146942.
LAWRENCE G.L., NICHOI
"Human herpesvirus 6
                                                                                 petween
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                                                                                SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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Similarity 53.3%;
8; Conservative
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                                                                                                                                                                                                                NICHOLAS J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                          ROSEOLOVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89553 MW;
                                                                                                                                                                                       LAS J., BARRELL B.G.;
(strain UllO2) encodes homologues of the
s glycoprotein gM and the alphaherpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                             CREATED)
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ANNOTATION UPDAT
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Pred. No. 4.27e-01;
2; Mismatches 5
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STAGE;
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                                                                                                                                                      REPLICATION.
                                                                                                                                 GROUPS TOGETHER
                                                                                                                                                                                                                                                                                               JONES M., THOM
MACAULAY H.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC32
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                                                                                                                                                                                                                                                                                     structure,
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European Bioinformatics Institute. The by non-profit institutions as long

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Best Local Similarity 53.3%;
Matches 8; Conservative
               EMBL; L33779; G1017465; -.
EMBL; L33779; G498019; -.
EMBL; X13885; G439671; -.
MGD; MGI:103221; DSC2,
MGD; MGI:103221; CADHERIN; 3
PROSITE; PS00223; CADHERIN; 3
PFAM: PP00028; Cadherin; 4.
HSSP; P09803; 1EDH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSC2_MOUSE STAN

P55292; O64734;

O1-OCT-1996 (REL. 3

O1-OCT-1996 (REL. 3

O1-NOV-1997 (REL. 3

DESMOCOLLIN 2A/2B F
                                                                                                                                                                                                                                                                                                                   JENKINS N.A., GILBERT D.J., COPELAND N.G.;

JENKINS N.A., GILBERT D.J., COPELAND N.G.;

MOUSE desmocollin (Dsc3) and desmoglein (Dsg1) genes are closely
linked in the proximal region of chromosome 18.";

GENOMICS 21:510-516(1994).

-i- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVE
IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS
MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO EPIDERMAL CELL
POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL
ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENTIAL
ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENTIAL
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I- TISSUE SPECIFICITY: IN ALL EPITHELIA TESTED AND HEART.
-I- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                                                                                               modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSC2 OR DSC3.

MUS MUSCULUS (MOUSE).

EUKARYOTA; METAGOA; CHORDATA; VERTEBRATA; MAMMALIA;

EUKARYOTA; METAGOATHI: MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                      ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning, sequence analysis and expression pattern of mouse desmocollin 2 (DSC2), a cadherin-like adhesion molecule."; MOL. MEMBRANE BIOL. 11:229-236(1994).
                                                                                                                                                                                                                                                                                                  <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BUXTON R.S., WHEELER G.N., PIDSLEY S.C., MINISTER N.A., GILBERT D.J., COPELAND N.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 344-637 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GARROD D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 95227276.
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DNA REPLICATION; DNA-BINDING; ATP-BINDING.
NP_BIND 52 59 ATP (POTENTIF
SEQUENCE 780 AA; 89716 MW; 5F096841 CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
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JEQUENCE FROM N.A.
---- CETRL/6; TISSUE-EMBRYO;
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                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS: FORMS 2A AND 2B ARE PRODUCED E SPLICING OF THE SAME GENE.
SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS
                                                                                                                                                                                       European Bioinformatics Institute.
                                                                                                                                                                                                                                                   DESMOSOMAL SUBFAMILY.
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GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-EMBRYO;
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34, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
PRECURSOR (EPITHELIAL TYPE
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Pred. No. 4.27e-01;
2; Mismatches 5
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TRANSMEM
DOMAIN
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EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
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CHAIN
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PROSITE; PS01230; TRMA_1; 1.
PROSITE; PS01231; TRMA_2; 1.
HYPOTHETICAL PROTEIN; HYDROLASE;
                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                          use by non-profit institu modified and this statement
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SUBMITTED (OCT-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
-!- SIMILARITY: TO YEAST ENDO-EXONUCLEASE NUCR (RNC.)
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                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffed and this statement is not removed. Usage by and for commercial
ECPIATKTINEEXP
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Pred. No.
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Pred. No. 4.27e-01;
2; Mismatches 3
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CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
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DESMOCOLLIN 2A,
EXTRACELLULAR
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MISSING (IN FORM 2B).
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CYTOPLASMIC
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5852EB45 CRC32;
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6.94e-01
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IN CHROMOSOME
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P41004;
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P55284;
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EUKARYQTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
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MUS MUSCULUS (MOUSE).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;

EUKARYOTA; METAZOA; CHORDATA; WORINAE;
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MEDLINE; 96141083.

BREIER G., BREVIARIO F., CAVEDA L., BERTHI GOTSCH U., VESTWEBER D., RISAU W., DEJANA "Molecular cloning and expression of murir cadherin in early stage development of cat BLOOD 87:630-641(1996).
                                                                                                                                                                                                                                                                                                                                                CDH5
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01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN)
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                                                                                                                                                                         TISSUE-BRAIN CAPILLARY;
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4; Mismatches 4
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                                   , BERTHIER R., SCHNUI
DEJANA E.;
of murine vascular en
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                                                                                                                                                                                                                                                                MAMMALIA;
MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAKEUCHI M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1324;
                                                                                                                    SCHNUERCH
                                                                                                                                                                                                                                                                                              EUTHERIA;
                                                                    endothelial-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restrictions
                                                                                                                                                                                                                                                                                                                                                                                 (CADHERIN-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a collaboration
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   RAP RAC OCCUPANT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -
                                                                                                                                                        01-OCT-1993
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                           CAD5_HUMAN P33151;
                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
REPEAT
REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00028; cadherin; 5.
PFAM; PF01049; Cadherin_C_term;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:105057; CDH5.
PROSITE; PS00232; CADHERIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION:
-!- SIMILARITY: BELONGS T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
SEQUENCE FROM N.A.
TISSUE-ENNOTHELIAL CELLS;
MEDLINE; 95353875.
BREVIARIO F., CAVEDA L., CORADA M., MARTIN-PADURA I., NAVARRO BREVIARIO F., CAVEDA L., CORADA M., MARTIN-PADURA I., NAVARRO GOLAY J., INTRONA M., GULINO D., LAMPUGNANI M.G., DEJANA E.;
"Functional properties of human vascular endothelial cadherin
                                                                                                                                           01-OCT-1993 (REL. 27, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                           OMOH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALCIUM-BINDING;
                                                                                   PRIMATES; CATARRHINI;
                                                                                             EUKARYOTA;
                                                                                                                                   (7B4 ANTIGEN) (CD144
                                                                                                                                                                                                                                                                             243 IRLEDINDNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES. THIS CADHERIN MAY PLAY A IMPORTANT ROLE IN ENDOTHELIAL CELL BIOLOGY THROUGH CONTROL OF THE COHESION AND ORGANIZATION OF THE INTERCELLULAR JUNCTIONS. NERVOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN
                                                                                                                                                                                                                                                       5 IKVKDVNDNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P09803; 1EDH.
ADHESION; GLYCOPROTEIN; PHOSPHORYLATION;
                                                                                                SAPIENS (HUMAN).
RYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          x83930;
                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                                                                                      Conservative
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619
783
148
255
370
370
475
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752
752
753
87847
                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT;
                                                                                                                                                                                                                                                       15
                                                                                                                                                                                                                                                                              253
                                                                                                                                                                                                                                                                                                                 50.4%;
                                                                                                                                    ANTIGEN).
                                                                                      HOMINIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N: TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
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                                                                                                                                                                                                                                                                                                Score 57; DB 1; Le
Pred. No. 1.12e+00;
3; Mismatches 1;
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VASCULAR ENDOT
EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                           CADHERIN
SER-RICH.
                                                                                                                                                                                                                                                                                                                                                  POTENTIAL:
DOB71215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CADHERIN
CADHERIN
                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CADHERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I MEMBRANE PROTE CADHERIN FAMILY.
                                                                                                VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                          PRT;
                                                                                      OWOH
                                                                                                                                                                                                           784
                                                                                                                                                                                                                                                                                                                                                                                                                                         54 ω 2 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENDOTHELIAL-CADHERIN
LULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                       CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                           B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                              Length 783
                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADHESION PROTEINS
                                                                                                 EUTHERIA,
                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                          Gaps
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DOMAIN
CARBOHYD
CARBOHYD
CARBOHYD
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**SUZUKI'S., SANO K., TANIHAP

**Diversity of the cadherin

**The cadherin cadh
                                                                                                                                                                                                                                    TRANSMEM
DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                       PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. CELL BIOL. 118:1511-1522(1992).

-!- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

-!- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

-!- THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES. THIS CADHERIN MAY PLAY A IMPORTANT ROLE IN ENDOTHELLAL CELL BIOLOGY THROUGH CONTROL OF THE COHESION AND ORGANIZATION OF THE INTERCELLULAR JUNCTIONS. IT ASSOCIATES WITH ALPHA-CATENIN FORMING A LINK TO THE CYTOSKELETON.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. FOUND AT CELL-CELL BOUNDARIES.

-!- TISSUE SPECIFICITY: ENDOTHELIAL TISSUES AND BRAIN.

-!- SIMILARITY: BELONGS TO THE CADHERIN FORMILY.
                                                                                                                           REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X79981; G599834; -. EMBL; U84722; G1814076; -- EMBL; X59796; G29593; -. PIR; S24305; IJHUC5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAMPUGNANI M.G., RESNATI M., RAITERI M.
HOUEN G., RUCO L.P., DEJANA E.;
"A novel endothelial-specific membrane
cell-cell contacts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00028; cadherin; 5.
PFAM; PF01049; Cadherin_C_term;
HSSP; P09803; 1EDH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALI J., MULLER W.;
SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL ADHESION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 601120; -.
PROSITE; PS00232; CADHERIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARTIAL SEQUENCE
                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                  CALCIUM-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-ENDOTHELIAL CELLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 5-784 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (7B4/cadherin-5), an endothelium-specific cadherin.";
RTERIOSCLER. THROMB. VASC. BIOL. 15:1229-1239(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATABASE: NAME-PROW; NOTE-CD guide CD144 entry; www-"http://www.ncbi.nlm.nih.gov/prow/cd/cd144.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Ex-
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                                                                                                                                                                                                                                                                                                                                                                                                                                          GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TANIHARA H.;
adherin family:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ω
·
                                      POTENTIAL.
CYTOPLASMIC
CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
SER-RICH.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAITERI M., PIGOTT R.,
                      POTENTIAL.
                                                                                                                                                                                                                                                                                                   VASCULAR ENDOTHELIAL-CADHERIN EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        evidence for eight new cadherins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein is a marker of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PISACANE A.,
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Best Local
ALTERNATIVE
SIGNAL
PROPEP
CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                               PARKER A. E., WHEELER G.N., ARNEMANN J., PIDSLEY S.C., ATALIOTIS P., THOMAS C.L., REES D.A., MAGEE A.I., BUXTON R.S.;
"THOMAS C.L., REES D.A., MAGEE A.I., BUXTON R.S.;
"Desmosomal glycoproteins II and III. Cadherin-like junctional molecules generated by alternative splicing.";
J. BIOL. CHEM. 266:10438-10445(1991).
1- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLIN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENT IN THE INTERACTION DHESION. MAY CONTRIBUTE TO EPIDERMAL CELL POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL CELL ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS.
1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
1- TISSUE SPECIFICITY: EXPRESSED IN EPITHELIA, MYOCARDIUM AND LYMP
                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSC2_HUMAN
Q02487;
Q1-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
                                                                 PFAM; PF00028; cadherin; 4. HSSP; P09803; 1EDH. CELL ADHESION; GLYCOPROTEIN;
                                                                                                                                                    EMBL; X56807; G30508;
EMBL; X56807; G30509;
PIR; B40390; IJHUDA.
                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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HOMO SAPIENS (HUMAN).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994 (REL.
01-NOV-1997 (REL.
DESMOCOLLIN 2A/2B
                                                                                              PROSITE; PS00232; CADHERIN; PFAM; PF00028; cadherin; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-KERATINOCYTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIMATES; CATARRHINI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 IKVHDVNDNWP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESMOCOLLIN-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 IKVKDVNDNFP 15
                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
ALTERNATIVE PRODUCTS: TWO FORMS; 2A OR DGII DGIII; ARE PRODUCED BY ALTERNATIVE SPLICING SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
                                                                                                                          , A40390;
, 125645;
                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                                                                                                                                                                                                                                                                                        DESMOSOMAL SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                           NODES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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SPLICING; C

1: 27

28 135

136 901

136 694
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535
                                                                                                                                        IJHUDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             442
523
535
517
87528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28, CREATED)
28, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
PRECURSOR (DESMOSOMAL GLYCOPROTEIN II AND III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.4%;
                                                                                                                                                               ALT_INIT.
                                     ROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL;
CYTOSKELETON; CALCIUM-BINDING; PHOSPHORYLATION.
7
POTENTIAL.
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Pred. No. 1.12e+00;
0; Mismatches 2
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I -> T (IN
C2C5CD71
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DESMOCOLLIN 2A/2B.
EXTRACELLULAR (POTENTIAL)
                           POTENTIAL.
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FT TRANSMEM 695 715 POTENTIAL.
FT DOMAIN 716 901 CYTOPLASMIC (POTENTIAL).
FT REPEAT 144 355 CADHERIN 1.
FT REPEAT 244 355 CADHERIN 2.
FT REPEAT 356 471 CADHERIN 3.
FT REPEAT 36 471 CADHERIN 3.
FT REPEAT 36 471 CADHERIN 3.
FT REPEAT 390 694 CADHERIN 3.
FT CARBOHYD 34 34 POTENTIAL.
FT CARBOHYD 166 166 POTENTIAL.
FT CARBOHYD 546 546 POTENTIAL.
FT CARBOHYD 546 546 POTENTIAL.
FT CARBOHYD 629 629 POTENTIAL.
FT CARBOHYD 629 629 POTENTIAL.
FT CARBOHYD 629 629 POTENTIAL.
FT WOD_RES 864 864 PHOSPHORYLATION (POTENTIAL).
FT VARSPLIC 848 901 MV; CB68FC4 CRC32;

QUETY MAtch
Best Local Similarity 53.8%; Pred. No. 1.12e+00;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 341 CIINIDDVNDHLP 353
| 1 :: | | | | | | | | | |
QU 3 CNIKVKDVNDNFP 15
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Search completed: Fri Jun 11 17:36:19 1999 Job time: 8 secs.

Scoring table:	Title: Description: Porfect Score: Sequence:	Run on: Tabular outp	MPsrch_pp	C R	* * * * * * * * * * * * * * * * * * *
Le: PAM 150 Gap 15	>US-08-991-628-5 : (1-15) from US08991628.pep re: 113 1 CECNIKVKDVNDNFP 15	Run on: Fri Jun 11 17:36:36 1999; MasPar time 6.12 Seconds 133.859 Million cell updates/sec Tabular output not generated.	protein - protein database search, using Smith-Waterman algorithm	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	

searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb19

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 25.706; Variance 33.200; scale 0.774

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

11	Result No.
107 663 663 677 677 677 677	Score
94.7 57.5 57.5 55.8 55.8 55.8 53.1 53.1 53.1 50.4 4.9 50.4 6.8 6.8 6.8 6.8 6.8 6.8 6.8 6.8 6.8 6.8	Query Match
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DESMOGLEIN 3 (FRAGMENT HYPOTHETICAL 25.1 KD P VENTRAL NEURAL CADHERI METHYLVTOLOGEN - REDUCIN R11A8.7 PROTEIN. CO2D4.2 PROTEIN. CO2D4.2 PROTEIN. SYNAPSIN S-SYN-LONG (F SYNAPSIN S-SYN-LONG (F DESMOCOLLIN TYPE 2 (FR REPLICATION ORIGIN-BIN SIMILARITY TO MULTIPLE MIC CLASS I PRECURSOR. INTESTINAL PEPTIDE-ASS LI-CADHERIN. PEPTIDE SYNTHETASE. DAR REPLICATION PROTEI CADHERIN-5. KIDNEY-SPECIFIC CADHER R05H10.6 PROTEIN.	Description
4.84 6.344 7.032 7.032 7.032 7.032 7.032 7.032 7.032 7.032 7.032 7.032 7.032 7.032 7.032 7.032 7.032	Pred. No.

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MANNOSE 6-PHOSPHATE/IN	POLYPROTEIN (FRAGMENT)	MITOCHONDRIAL ATP9 GEN	VARIABLE MAJOR PROTEIN	TPH-TRYPTOPHAN HYDROXY	HYPOTHETICAL 206.5 KD	K12C11.4 PROTEIN.	POTASSIUM CHANNEL (FRA	493AA LONG HYPOTHETICA	B0281.8 PROTEIN.	G-CADHERIN.	CARBOXYPEPTIDASE GP180	CARBOXYPEPTIDASE D.	CADHERIN HOMOLOG.	T27E13.16 PROTEIN.	KSP-CADHERIN.	KIAA0345-LIKE 13.	CHAPERONE DNAJ.	296AA LONG HYPOTHETICA	HYPOTHETICAL 27.9 KD P	BETA4 - INTEGRIN.	BETA4 - INTEGRIN.	BETA4 - INTEGRIN.	INTEGRIN VARIANT BETA4	POTASSIUM CHANNEL (AKT
1.65e+01	1.65e+01	1.65e+01	1.65e+01	1.65e+01	1.07e+01	1.07e+01	1.07e+01	1.07e+01	1.07e+01	6.90e+00	6.90e+00	6.90e+00	6.90e+00	6.90e+00	6.90e+00	6.90e+00	6.90e+00	6.90e+00	6.90e+00	4.42e+00	4.42e+00	4.42e+00	4.42e+00	4.42e+00

ALIGNMENTS

PRT; 993 AA. REATED) AST ANNOTATION UPDATE) AST ANNOTATION UPDATE) E; MUS. TRANSMEMBRANE; CALCIUM-BINDING; REPEAT. REATED) COOPE 107; DB 11; Length 993; Fred. No. 4.84e-12; Fred. No. 4.84e-12; Fred. No. 4.84e-12; Fred. No. 4.84e-12; CISEAUENCE UPDATE) AST ANNOTATION UPDATE) AST ANNOTATION UPDATE) C16E8.02 IN CHROMOSOME I. SSION YEAST). ARCHHASCOMYCETES; CJOSACCHAROMYCETACEAE;

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RESULT

ID Q90425

AC Q90425;

C Q90425;

DT 01-NOV-1996 (TREMBLREL 01, CREATED)

DT 01-NOV-1996 (TREMBLREL 08, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)

DT 01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)

DT 01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)

OC CHARYOTA; METAZOA; CADHERIN (FRAGMENT).

OC GUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII

OC CYPELIDAR; METAZOA; CHORDATA; VERTEBRATA; CYPRINIFORMES; CYPRINOIDEA;

KN (1)

CC CYPELIDAE; RASBORINAE; DANIO.

KN (1)

RP SEQUENCE FROM N.A.

FRANKLIN J.L., SARGENT T.D.;

RL DEV. DYN. 2060-0(0).

CG -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

DR PROSITE; MENGLE; CADHERIN; 1.

DR PROSITE; PS00232; CADHERIN; 1.

PFAM; PFO0028; CADHERIN; 1.

PFAM; PFAM; PFO0028; CADHERIN; 1.

PFAM; PFAM; PFO0028; CADHERIN; 1.

PFAM; PFAM
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HYPOTHETICAL PROTEIN; TRANSMEMBRANE.

T TRANSMEM 28 48 POTENTIAL.

T DOMAIN 31 34 POLY-LEU.

TOMAIN 66 86 POTENTIAL.

FT TRANSMEM 106 126 POTENTIAL.

FT TRANSMEM 106 126 POTENTIAL.

FT TRANSMEM 136 156 POTENTIAL.

TRANSMEM 136 156 POTENTIAL.
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Q1-AUG-1998 (TREMBLREL, 0:
Q1-AUG-1998 (TREMBLREL, 0:
Q1-NOV-1998 (TREMBLREL);
Q1-NOV
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STRAIN-972;
OLIVER K., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WOOD V.;
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL)
-!- SIMILARITY: TO YEAST YGLOLOW AND SOME, TO N.CRASSA ATP-6.
   SEQUENCE FROM N.A. STRAIN-DSM 2661;
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4 NIKVKDVNDNFP
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Similarity 91.7%;
11; Conservative
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Similarity 66.7%;
8; Conservative
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07, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
HYDROGENASE POLYFERREDOXIN PROTEIN.
                                                                                                                                         METHANOCOCCALES; METHANOCOCCACEAE;
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Pred. No.
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No. 6.34e-02;
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. 6.34e-02;
----hes 1;
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83

CPIGIKKVDDDFP CNIKVKDVNDNFP

95

Query Match Best Local S Matches

Similarity

55.8%; larity 53.8%; Conservative

Score Pred. 3; N

re 63; DB 1; L. 1. No. 1.68e-01; Mismatches 3

Length 394;

0,

Gaps

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RX MEDLINE; 96337999.

RA SUTTON G.G., BLAKE J.A., FITZCERALD L.M., CLAYTON R.A., GOCANNE J.D.,

RA SUTTON G.G., BLAKE J.A., FITZCERALD L.M., CLAYTON R.A., GOCANNE J.D.,

RA KERLAVAGE A.R., DOUGHERIY B.A., TOND J.-F., ADAMS M.D., REICH C.I.,

RA OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,

RA SCOTT J.L., GEDGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,

RA COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORDOVSKY M.,

RA COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORDOVSKY M.,

RA KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;

RA KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;

RT "Complete genome sequence of the methanogenic archaeon, Methanococcus

RT Jannaschil.", S8-1073(1996).

RE SCIENCE 273:1058-1073(1996).

C. -!- FUNCTION: FERREDOXINS ARE IRON-SULFUR PROTEINS THAT TRANSFER

CC -!- FUNCTION: SEVERAL REPEABOLIC REACTIONS.

C. -!- THIS PROTEIN CONTAINS SEVERAL REPEABOLIC REACTIONS.

C. -!- SUBUNIT: VHU CONSISTS OF THE VHUA, VHUG, VHUU SUBUNTS AND A

FERREDOXIN PROTEIN.
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PROSITE; PS00198; 4FE4S_FERREDOXIN; PFAM; PF00037; fer4; 6.

ELECTRON TRANSPORT; IRON-SULFUR: REF
     SEQUENCE
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DI Q21920;
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DI O1-NOV-DI ONNE O1-NOV-DI ONNE
STRAIN-NO./;

{ MEDLINE; 97214635.

A MOMMA K., INUI M., YAMAGATA H., YUKAWA H.;

A "Cloning of dnaK and dnaJ homologous genes fro bacterium Rhodopseudomonas species.";

BIOCHIM. BIOPHYS. ACTA 1350:235-239(1997).

CC ... ISIMILARITY: TO OTHER PROKARYOTIC DNAJ, AN CCC DNAJ-LIKE PROTEINS.

CC DRAJ-LIKE PROTEINS.

CR EMBL; D78133; D1020582; -...

DR EMBL; D78133; D1020582; -...
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Best Local :
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MEDLINE; 94150718.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., WILSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON R. BONFIELD J., BURTON J., COURBIN R., FAVELLO A., FULTON L., CANTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., CANTON R., CREEN R., LATREILLE P., JOHNSTON L., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN S., SAUNDON J., SNITH A., SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

"2.2 Mb of contiguous nucleotide sequence from chromosome III of C."
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01-JUL-1997
01-NOV-1998
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EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q21920; Q21927;
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
01-JAN-1999 (TREMBLREL.
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(TREMBLREL.)
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BONFIELD J., BURTON J., CONNELL M., COPSET J., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., KCMURRAY A., MORIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN )
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VANDIN M., VAUGHAN K., WATERSTON R.,
WEINSTOCK L., WILKINSON-SPROAT J., WOLLDMAN P.;
"3.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE, PS00637; DNAJ_CXXCXGXG; PRAM; PF000226; DNAJ; 1.
PFAM; PF00684; DNAJ_CXXCXGXG; 1.
CHAPERONE; DNA REPLICATION.
                                01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
SYNAPSIN S-SYN-SHORT (FRAGMENT).
LOLIGO PEALEII (LONGFIN SQUID).
EUKARYOTA; METAQQA; MOLLUSCA; CEPHALOPODA; COLEOIDEA; TEUTHOIDA;
                                                                                                                                                                                                                                                                                                                 NATÜRE 368:32-38(1994).

1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY EMBL; Z81031; E1343679; -..
PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
SEQUENCE 501 AA; 56404 MW; 18F1C57F CRC32;
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01-JUL-1997 (TREMBLREL.
01-AUG-1998 (TREMBLREL.
C02D4.2 PROTEIN.
                                                                                                                          076322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA;
RHABDITINA; RHABDITOIDEA; RHAI
                          LOLIGO PEALEII (LONGFI)
EUKARYOTA; METAZOA; MOJ
MYOPSIDA; LOLIGINIDAE;
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A REPLICATION.
9 AA; 40992 MW;
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38.58;
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RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
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LAST SEQUENCE UPDATE)
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Pred. No. 2.72e-01;
5; Mismatches (
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SEQUENCE
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EUKARYOTA; METAZOA; CHORDATA; VI
CARNIVORA; FISSIPEDIA; CANIDAE;
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           EUR. J. CELL BIOL. 76:192-203(1998).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PR
EMBL; AJ002299; E1315148; -.
PROSITE; PS00232; CADHERIN; 3.
CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE;
                                                                                                                                                                      MEDLINE; 98380
ROBERTS G.A.,
                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 98380123.
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Neurotransmitter Release
SUBMITTED (MAR-1998) TO F
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EUKARYOTA; METAKOA; MOLLUSCA; CEPHALOPODA; COLEOIDEA;
MYOPSIDA; LOLIGINIDAE; LOLIGO.
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Neurotransmitter Release."
SUBMITTED (MAR-1998) TO EMEL; AF055373; G3273724;
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Similarity 35.7%;
5; Conservative
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LAST SEQUENCE UI
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Pred. No. 7.03e-01
4; Mismatches
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                                                                                 BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULS CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATEFILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN I PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKI SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON B., WATESON A., WEINSTOCK I., WITTYYOO.
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE; 94150718.
WILSON R., AINSCOUGH F
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01-JUL-1997
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Q69468
Q69468;
                                 THIERRY-MIEG J., THOMAS I WATSON A., WEINSTOCK L., "2.2 Mb of contiguous nuclearans.";
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EMBL; Ul3194; G662096; -.
NON_TER 1 1 1
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VIRUSES; DSDNA VI
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5 (TREMBLREL. 01,
3 (TREMBLREL. 08,
N ORIGIN-BINDING P
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No. 7.03e-01
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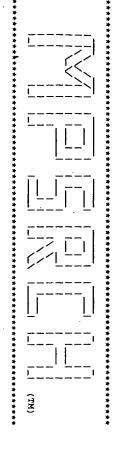
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SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
DU Z., GATTUNG S.;
SUBMITTED (MAY-1997) T
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01-MAY-1997 (TREMBLREL.
01-JAN-1999 (TREMBLREL.
MHC CLASS I PRECURSOR.
ONGO 92H.
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P79570
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01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMBLEL. 08, LAST ANNOTATION UPDATE)
INTESTIALL PEPTIDE-ASSOCIATED TRANSPORTER HPT-1.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MANMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KATAGIRI T., HIRONO I., AOKI T., SAKAI "ISOLATION OF major histocompatibility salmon (Oncorhynchus gorbuscha).";
DEV. COMP. IMWUNOL. 20:217-228(1996).
EMBL; D58386; D1010199; -.
PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
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SUBMITTED (MAY-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ONCORHYNCHUS GORBUSCHA (PINK SALMON) (HUMPBACK SALMON).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORME:
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                      CATARRHINI; HOMINIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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KATAGIRI T., HIRON
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Local Similarity 53.3%;
Local Similarity 53.3%;
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Similarity 38.5%;
5; Conservative
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339 AA;
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9 (TREMBLREL.
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38268 MW;
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Pred. No. 1.12e-
3; Mismatches
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1.78e+00;
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A JENKINS I.L., DUCKWORTH D.C., SPORTSMAN R., MACKENSEN D.,
A ROSTECK P.R., SKATRUD P.L.,
T "Association of intestinal peptide transport with a protein relation to the cadherin superfamily.";
SCIENCE 264:430-433(1994).
C -!- SUCCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY EMBL; U07969; G483392; -.
R EMBL; U07969; G483392; -.
R PROSITE; PS000232; CADHERIN; 3.
R PROSITE; PS000232; CADHERIN; TRANSMEMBRANE; CALCIUM-BINDING; REP.
CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; CALCIUM-BINDING; REP.
CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; CALCIUM-BINDING; REP.
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                                                                                                                                                                                BOETTINGER A., KREFT B., FIEGER C., DLOUHY
GOESSNER R., TAUBER R.;
SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE
                                                                                                                                                                                                                                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                             PFAM; PF00028; cadherin; 6.
CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; CALCIUM-BINDING; SEQUENCE 832 AA; 92207 MW; 65C92D4C CRC32;
                                                                                                                                                     EMBL; X83228; G854175; -. PROSITE; PS00232; CADHERIN; 3.
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                325 EIHVKVKDINDNPP 338
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Similarity 64.3%;
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3; Mismatches 2
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LAST SEQUENCE UPDATE)
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Pred. No. 1.78e+00;
3; Mismatches 2
                                                                                                                                                                                                                                                                                    VERTEBRATA; MAMMALIA;
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Release 3.1A John F. Collins; Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U Distribution rights by Oxford Molecular Ltd Unit.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:45:41 1999; MasPar time 7.95 Seconds 40.150 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: 109 >US-08-991-628-6
(1-15) from US08991628.pep

Sequence: SARTLNNRYTGPYTF 15

Scoring table: PAM 150 Gap 15

170751 seqs, 21266608 residues

Post-processing: Minimum Minimum Match 0% Listing first 45 summaries

geneseq35

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7: 8:part8 9:part9 10:part10 11:part11 12:part12 13:p 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38 part39 13:part13 7:part7

Statistics: Mean 19.152; Variance 58.684; scale 0.326

Pred. No. score grea greater t s derived is the number of he number of results predicted by chance to have a than or equal to the score of the result being printed, by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	Б	Description	Pred. No.
1	109	100.0	15	20	W04846	Self epitope of desmo	5.33e-05
N	109	100.0	614	19	W07908	Pemphigus vulgaris an	5.33e-05
ω	109	100.0	999	σ	R30742	phigus	•
4	56	51.4	480	N	R12099	Haem 84-2 portion of	6.15e+01
S	56	51.4	516	Ŋ	R12098	Haem 84-1 portion of	6.15e+01
O	55	50.5	431	17	R97293	Mouse CRF RB1 recepto	7.81e+01
7	54	49.5	91	w	P61040	N-terminal region of	9.89e+01
œ	54	49.5	246	œ	R40924	Protein able to bind	9.89e+01
9	54	49.5	428	22	W08609	Chimeric MoMLV and Ty	9.89e+01
10	54	49.5	429	22	W08606	and	9.89e+01
11	54	49.5	431	15	R90575	Rat CRF2-beta recepto	9.89e+01
12	54	49.5	449	22	W08608	Chimeric MoMLV and Ty	9.89e+01
13	54	49.5	1196	16	R75189	Osteoinductive retrov	9.89e+01
14	53	48.6	105	21	W00832	Variable light chain	1.25e+02
15	53	48.6	105	24	W19018	Anti-human FasL antib	1.25e+02
16	53	48.6	653	7	R37425	IDUA.	1.25e+02

45	44	43	42	41	40	39	38	37	36	ω 5	34	ω ω •.	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	1/
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2516	84	30	845	687	548	548	129	128	128	128	128	127	108	107	106	45	39	50	2504	84	84	691	454	454	105.	105	2205	۲
25	<u>ω</u>	34	31	σ	29	10	13	10	36	ü	36	20	ഗ	ഗ	œ	G	u	3	25	25	Ω	N	18	17	29	29	5	3
789	5657	W68155	57	207	662	401	R70256	521	w	025	43	44	R28751	₽	956	u	510	655	787	830	UT.	71		361	224	W52241	R79048	176
rhabdus	Toxin TcdAii, encoded	Human angiotensin con	Fragment of toxin Tcd	Bovine transglutamina	Amino acid sequence o		Anti-VLA-4 humanized			ted V	1sed	VL region BR	Light chain variable	chain	ence of t	prodrug	prodrug analogu	Toxin TcbA, encoded b	lumines	ıbdus i	ode	of gu	i's sarcoma ass	si's sa	7 LD1/2-6-	dy LD1/2-6-3	Infectious rubella vi	Ruberta Virus KAZ//3
.99e+	.99e+	1.99e+	1.99e+0	1.99e+0	1.99e+0	1.99e+0	.99e+0	.99e+0	.99e+0	.99e+0	.99e+0	.99e+0	1.99e+02	.99e+0	.99e+	.99e+0	.99e+0	.58e+0	.58e+0	.58e+0	.58e+0	.58e+0	.58e+0	.58e+0	.58e+0	. 58	. 25e	ï

ALIGNMENTS

SOUTH THE SULFACE OF THE SULF WE SEE THE SULF WE SULF derived from th Claim 1; Page 41; 58pp; English.

Pharmaceutical preparations for tolerisation to antigens comprise either an isolated human non-collagen or non-myslin basic protein (MBP) polypeptide which is capable of tolerising an individual to autoantigen; or an isolated human pathogen polypeptide capable of tolerising an individual to that polypeptide. In both cases, the polypeptide (whether self or non-self) includes an amino acid protein, such as HLA-DR, which is associated with a human autoimmune disease and which binds to the polypeptide to activate autoreactive T-cells in individuals with the autoimmune disease. This peptide is derived from the human desmoglein 3 protein (amino acids 512-526) and is implicated as a self epitope in pemphigus vulgaris. Peptides derived from the human desmoglein protein are described in W04841-47 Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens - useful in disease treatment, and method for identification of other self and non-self antigens implicated in Strominger JL, WWWPI; 96-425218/42 12-SEP-1996. 07-MAR-1996; U03182. 07-MAR-1995; US-400796. (HARD) HARVARD COLLEGE polypeptide (whether self or non-self) includes an amino ac sequence corresponding to a sequence motif for a MHC class auto-immune disease autoantigen; HLA; human leukocyte antigen; T-cell;
pemphigus vulgaris; desmoglein; multiple sclerosis; Self epitope of desmoglein 3, implicated in autoimmune disease Tolerisation; self-epitope; antigen; autoimmune disease; W04846 standard; peptide; 15 AA nerpes simplex virus; adenovirus; phosphomannomutase; numan papillomavirus; Epstein-Barr virus; DNA polymerase; 18-FEB-1997 (first entry) haemagglutinin; Wucherpfennig KW sigma protein thymocyte; an

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  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative
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27-NOV-1991; US-798918.
(USSH) US DEPT HEALTH & HI
Amagai M, Klaus-kovtun V,
WPI; 93-067436/08.
N-PSDB; Q35992.
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30-JUN-1995; 165632.
30-JUN-1994; JP-173291.
(NISH/) NISHUKAWA T.
WPI; 96-388562/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fused protein recognised by pemphigus vulgaris auto:antibody useful to treat and diagnose pemphis vulgaris
Claim 1; Page 7-9; 9pp; Japanese.
W07908 represents the human pemphigus vulgaris (PV) antigen extracellular region. The PV antigen is produced in patients with pemphis vulgaris resulting in autoimmune disease. PV is a rare relapsing disease causing suprabasal, intra-epidermal bullae (vesicles) of the skin and mucuous membranes, which is fatal if untreated. The PV antigen was fused to a human IgG1 hinge region and the resulting fusion protein is useful to treat or diagnose
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Pemphigus vulgaris antigen protein extracellular region.
Autoantibody; immunoglobulin G; IgGl; fusion protein; diagnosis;
treatment; pemphigus vulgaris; PV; bulla; blister; skin disease;
                                                                                                                                 DNA encoding pemphigus vulgaris antigen - useful in proteins for diagnostic and therapeutic uses Disclosure; Fig 7; SOpp; English.
This sequence is the pemphigus vulgaris 130kD antigen. The protein and its encoding DNA may be used in the diagnosis and treatment of pemphigus vulgaris. It is thought that the antigen may be a cell adhesion molecule.
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R30742;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human pemphigus vulgaris 130kD antigen.
Pemphigus vulgaris; skin disease; autoantibodies;
keratinocyte cell surface antigen; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo
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15; Conservative
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614 AA;
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V, Stanley JR;
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Pred. No. 5.33e-05;
0; Mismatches 0;
Score 109; DB 6;
Pred. No. 5.33e-05;
0; Mismatches 0
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17-SEP-1990; 062569.
18-SEP-1998; US-408339.
01-MAR-1990; US-487181.
(SYNE-) SYNERGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein from Haemonchus contortus and other nematodes therapeutic and prophylactic agent to protect plants, humans from parasitic nematode infection. Disclosure, Fig 49; 20pp; English. The proteins derived from the nematode DNA may be used vaccines against parasitic infection of plants, humans esp. sheep. MAbs may also be raised to provide passive prophylaxis against infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R12099
R12099;
                                                                                                                                Protein from Haemonchus contortus and other nematodes - used as therapeutic and prophylactic agent to protect plants, animals or humans from parasitic nematode infection.

Disclosure; Fig 49; 209p; English.

The proteins derived from the nematode DNA may be used to derive vaccines against parasitic infection of plants, humans and animals esp. sheep. MAbs may also be raised to provide passive therapy and prophylaxis against infection.
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01-MAR-1990; US-487181.
(SYNE-) SYNERGEN INC.
WPI; 91-133285/19.
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Parasitic nematode; vaccine;
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R12098;
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Claim 3; Page 83-85; 102pp; English.
Claim 3; Page 83-85; 102pp; English.
Mouse corticotropin releasing factor receptor mCRF-RB1 was
identified as the product of a cDNA clone (728972) isolated
mouse heart library. Recombinant mCRF-RB1 can be expressed
mouse heart library. Recombinant mCRF-RB1 can be receptor can
                                                                                                                                                                                                                                                                                                                                                                                         mouse heart library. Recombinant mCRF-RB1 can be expressed in host cells transformed by the cDNA clone. The receptor can be to identify agonists and antagonists that modulate the signal transduction activity mediated by CRF receptors. It may be administered therapeutically to reduce high ACTH levels caused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JUN-1996.
06-DEC-1995; U15909.
09-DEC-1994; US-353537.
17-ZAN-1995; US-374009.
(SALK ) SALK INST BIOLOGICAL STUDIES.
Chen R, Donaldson CJ, Lewis KA, Perrin
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                                         P61040 standard; Protein;
P61040;
03-JUL-1991 (first entry)
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by CRF-R
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levelop prods. for modulating signal transduction
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23-MAY-1984; JP-102685.
23-MAY-1984; JP-102685.
(SHLS) SHISEIDO KK.
WPI: 86-025462/04.
16-JUL-1997 (first entry)
16-JUL-1997 (first entry)
16-JUL-1997 (first entry)
Chimeric MoMLV and Ty3 integrase designated AtBmCm.
Chimeric MoMLV and Ty3 integrated Entropy
MoLoney murine leukaemia virus; Saccharomyces cerevisiae;
MoLoney murine leukaemia virus; Saccharomyces cerevisiae;
retrotransposoni yeast Ty3; position specific integration;
inflammation; cardiovascular; autoimmune; cancer; HIV; haemophilia;
inflammation; cardiovascular; autoimmune; cancer; HIV; haemophilia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enzyme expression vector - giving transformant enzyme be used as host enzymes in polypeptide biosynthesis. Disclosure; Fig 4; 12pp; Japanese.
The vector may be used to express heterologous genes transformed host when galactose is added as a carbon Sequence 91 AA;
                                                                                                                                                                                                                                                                                  The synthetic gene encodes a protein corresponding to an antibody capable of binding to a specific antigen, in this case the HIV-1 tay protein. Many synthetic genes are synthesised, each containing a predetermined nucleotide region encoding the framework regions of the heavy and light chains of antibody and undetermined nucleotide regions which are random sequences. The genes are then used in the construction of vectors which are subsequently used to transform microbes. The proteins thus produced are screened for binding activity to the specific antigen.
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Antigen-binding proteins and constructed synthetically and
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(HOFF) HOFFMANN LA ROCHE
Dillon PJ, Rosen CA;
WPI; 93-274375/35.
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Claim 13; Page 22; 40pp; English.
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                                                                                        W08609 standard;
W08609;
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Similarity 42.9%;
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llarity 54.5%;
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                                                                                                                                                                                                                                           Length 246
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Best Local :
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28.W0V-1996; U06727.
10-MAY-1996; U06727.
22-MAY-1995; US-445466.
(CHIR ) CHIRON VIAGENE INC.
(REGC ) UNIV CALIFORNIA.
Bilachone VW, Dildine SL,
                                                                                                                                 W0806;
16.JUL-1997 (first entry)
Chimeric MOMIV and Ty3 integrase designated AmBtCm.
Chimeric Mourand Ty3 integrase designated AmBtCm.
Moloney murine leukaemia virus; Saccharomyces cerevisiae;
Moloney murine leukaemia virus; Saccharomyces cerevisiae;
retrotransposon; yeast Ty3; position specific integration;
retrotransposon; yeast Ty3; autoimmune; cancer; HIV; hae:
                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a specific example of a chimeric integrase made up of three domains from MoMLV and Ty3, with at least one domain derived from Ty3 integrase. This protein can direct integration of a vector construct into a defined region of a target eukaryotic genome. As part of gene delivery vehicles and transduction competent recombinant retroviral particles it can be useful in somatic and germ cell gene therapy (in vivo or ex vivo) of a wide range of genetic, infectious, degenerative, inflammatory, cardiovascular and autoimmune diseases or cancer. Typical examples of the many potential applications include treatment of HIV infection, haemophilia, Alzheimer's disease and rheumatoid arthitis. This protein rather than wild-type retroviral integrase reduces the rate of insertional mutagenesis and the degree of variation in gene expression, and particularly does not disrupt that a cancer expression.
                                                                                                                                                                                                            T 10
W08606 standard;
                                                                                                                                                                                                                                                                                                                                                                                    tRNA gene expression.
N.B. The present sequence is made up from the two original
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                                                                                                  Alzheimer's disease; rheumatoid arthritis; chimeric. Chimeric - Moloney murine leukaemia virus.

Chimeric - Saccharomyces cerevisiae transposon Tv3.
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                                                                                                                                                                                                                                                                                                              Conservative
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/label = C
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42..284
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                                                                                      Location/Qualifiers
                                                                                                                                                                                                              protein;
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/note= "From MoMLV"
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l sequences as
                                                   MOMLV"
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No. 9.89e+01;
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therapy, providing
rates of insertions
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                                                                                                                                                                                                                                                                                                                                                                                     specified, MOMLV
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Claim 7; Page -; 98pp; English.

The present sequence is a specific example of a chimeric integrase made up of three domains from MoMLV and Ty3, with at least one domain derived from Ty3 integrase. This protein can direct integration of a vector construct into a defined region of a target eukaryotic genome. As part of gene delivery vehicles and transduction competent recombinant retroviral particles it can be useful in somatic and germ cell gene therapy (in vivo or ex vivo) of a wide range of genetic, infectious, degenerative, inflammatory, cardiovascular and autoimmune diseases or cancer. Typical examples of the many potential applications include treatment of HIV infection, haemophilia, Alzheimer's disease and rheumatoid arthritis. This protein rather than wild-type retroviral integrase reduces the rate of insertional mutagenesis and the degree of variation in gene expression, and particularly does not disrupt
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Best Local
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Sandmeyer SB;
WPI; 97-021229/02.
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eukaryotic genomes - useful for gene
consistent gene expression and lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.B. The present sequence is not shown in t
made up from the two original sequences as
which are shown.
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22-MAY-1995; US-445466.
(CHIR) CHIRON VIAGENE INC.
(REGC) UNIV CALIFORNIA.
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Similarity 46.2%;
6; Conservative
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245..261
/label=
262..286
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/note= "From MoMVL"
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                 Extracellular_domain
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9.89e+01;
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Best Local s
Matches
                                  28-NOV 1996.
28-NOV 1996; U06727.
10-MAY-1995; U05-445466.
22-MANY-1995; US-445466.
(CHIR ) CHIRON VIAGENE INC.
(REGC ) UNIV CALIFORNIA.
Tilachone VW, Dildine SL,
  Bilachone VW,
Sandmeyer SB;
WPI; 97-021229
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21-DEC-1995.
14-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corticotropin-releasing factor-2 receptor, and DNA encoding it used to isolate CRF-2 receptor antagonists for the treatment of resperovascular disorders, memory disorders and Alzheimer's dispisclosure; Page 63-66; 109pp; English.

Rat corticotropin-releasing factor-2-beta (CRF2-beta) receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding cDNA (T12244) in procaryotic or eucaryotic host cells. Recombinant CRF2 receptor is used to screen CRF2 receptor agonists and antagonists of therapeutic appln., and to prepare antibodies which specifically bind to CRF2 receptors.
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14-JUN-1994; US-259959.
31-JAN-1995; US-381433.
07-JUN-1995; US-485984.
(NEUR-) NEUROCRINE BIOSCIENCES INC.
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(R90575) is a membrane-bound G-coupled protein receptor in
in signal transduction. It can be produced by expression
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                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae
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343..363
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310..329
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364..431
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/note= "From MoMLV"
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/note- "From Ty3"
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Pred. No. 9.
                                           Jolly DJ,
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9.89e+01;
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05-APR-1994; 411718.
05-APR-1994; DE-411718.
(GSEU-) GSF FORSCHUNGSZENTRUM UMWELT
(GSEU-) GSF Wheel W, Oestergaard M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a specific example of a chimeric integrase made up of three domains from MoMIV and Ty3, with at least one domain derived from Ty3 integrase. This protein can direct integration of a vector construct into a defined region of a target eukaryotic genome. As part of gene delivery vehicles and transduction competent recombinant retroviral particles it can be useful in somatic and germ cell gene therapy (in vivo or ex vivo) of a wide range of genetic, infectious, degenerative, inflammatory, cardiovascular and autoimmune diseases or cancer. Typical examples of the many potential applications include treatment of HIV infection, hemophilia, Alzheimer's disease and rheumatoid arthritis. This protein rather than wild type retroviral integrase reduces the rate of insertional mutagenesis and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New chimeric integrase for targetted vector integration in eukaryotic genomes - useful for gene therapy, providing motionsistent gene expression and lower rates of insertional
1131 tknleprwkgpyt 1143
                                                                                                                                                 The full-length proviral genomic sequence of retrovirus RFB-14 has been determined. The virus codes for an osteoinductive protein, been determined the protein of the coding region has not yet been identified. The virus may be useful in gene therapy of bone growth
                                                                                                                                                                                                                                                                      Erfle V, Gimbel W,
Schmidt J, Strauss P;
WPI; 95-352078/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 trNA gene expression.

N.B. The present sequence is not shown in the specification, but is made up from the two original sequences as specified, MoMLV and Ty3, which are shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutagenesis
Claim 7; Page -;
                                                                                                  disorders such as osteoporosis. viral pol gene product. Sequence 1196 AA;
                                                                                                                                                                                                                   RFB-14 retrovirus genome - an
Claim 14; Fig 1; 46pp; German.
                                                                                                                                                                                                                                                      N-PSDB; Q94266.
                                                                                                                                                                                                                                                                                                                                                                                             DE4411718-A1.
                                                                                                                                                                                                                                                                                                                                                                                                         Retrovirus RFB-14.
                                                                                                                                                                                                                                                                                                                                                                                                                           reverse transcriptase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFB retrovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Osteoinductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   degree of variation in gene expression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381 tknleprwkgpyt 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ARTLNNRYTGPYT
                                                                                                                                                                                                                                                                                                                                                                                                                                           development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein; 1196 AA.
                               h 49.5%;
Similarity 46.2%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   449
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larity 46.2%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                       retrovirus RFB-14 pol gene product.
gag; pol; env; osteogenesis; osteoinductive protein;
t; osteoporosis; gene therapy; polymerase;
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                               Score 54;
Pred: No.
3; Misma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 54; DB 22;
Pred. No. 9.89e+01;
3; Mismatches 4
                                                                                                                                   The present sequence is that of the
                                                                                                                                                                                                                                   prodn.
                                   No. 9.89e-
Mismatches
                                                                                                                                                                                                                                                                                                      & GESUNDH
Pedersen
                                                                                                                                                                                                                                                                                                       GESUNDHEI.
Pedersen FS,
                                                  DB 16;
9.89e+01;
                                                                                                                                                                                                                                     of osteo-inductive proteins
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                                                                Length 1196;
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RESULT 14 ID W00832 : AC W00832;

standard; Protein; 105

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ARTLNNRYTGPYT

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Pl solution

Pl solution

Pl solution

Pl claim 28; Page 91; 133pp; Japanese.

CC The present sequence is the light chain variable region of the great sequence is the light chain variable region of the canti-human Fas ligand monoclonal antibody (WAb) NOK-5 NOK-5 is produced by the hybridoma NOK-5 (FERM BP-5048), which was prepared by immunising mice with transformed human Fas ligand expressing COS cells, and fusing spleen cells isolated from the mice with myeloma CC passlage 653 (ATCC CRL-1580) cells. The MAb recognises the human CC Fas ligand on the cell surface or in solution, and can be used to inhibit the apoptosis inducing cell surface Fas ligand/Fas reaction. The MAb can also be used for a Fas ligand assay in CC diagnosis, e.g. hepatitis, human blood), especially for disease CC lipus erythematosis.

So sequence 105 AA;
       Query Match
Best Local S
Matches
apoptosis in liver cells and improves liver function Claim 6; Page 41; Slpp; Japanese.
The present sequence is the light chain variable region of the murine anti-human Fas ligand (Fast) monoclonal antibody (MAb) NOK5, which is expressed by the hybridoma NOK5 (FERM BP-5044). The MAb can be used in the preparation of a composition for the effective oral or parenteral treatment of hepatitis, including hepatitis caused by hepatitis B or C virus. The composition controls apoptosis in liver cells caused by the binding of Fast to Fas expressing liver cells, and improves liver function by improving blood glutamate oxaloacetate and pyruvate transaminase levels. The composition is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JAN-1998 (first entry)
Anti-human Fasi antibody (NOK5) light chain variable region.
Light chain; variable region; mouse; murine; human; Fas ligand;
Fasi; monoclonal antibody; MAb; hybridoma; treatment; hepatitis;
hepatitis; B virus; HBV; hepatitis C virus; HGV; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SUME ) SUMITOMO ELECTRIC IND CO. Kayagaki N, Nakata M, Okumura K WBI; 96-443140/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Variable region; light chain; human; Fas ligand; mantibody; NOK-5; hybridoma; inhibition; apoptosis; disease; hepatitis; infectious mononucl
                                                                                                                                                                                                                                                                                                                                    (SUME ) SUMITOMO ELECTRIC IND CO. Kayagaki N, Nakata M, Okumura K, WPI; 97-258767/23.
                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1997.
24-OCT-1996; J03089.
27-OCT-1995; JP-303491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus sp.
W09715326-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibody specifically recognising the Fas ligand - useful for the detection of Fas ligands either on cell surface or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; T39558
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27-OCT-1995; JP-303492.
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Variable light chain of anti-human Fas ligand antibody NOK-5
                                                                                                                                                                                                                                                                             Anti-human Fas Ligand antibody to treat hepatitis - controls
                                                                                                                                                                                                                                                                                                            N-PSDB; T69542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W19018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W19018 standard; Protein; 105 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    iver cell; glutamate oxaloacetate; pyruvate transaminase.
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local Similarity 62.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 53; DB 21; Le
Pred. No. 1.25e+02;
3; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                        Seino K,
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                                                                                                                                                           were fused with mouse myeloma cells to produce hybridomas. The hybridomas were screened for anti-FasL activity, and the active clones NOK1-5 isolated.
                                                                                                                                                                                                given in a dosage of 0.0001-1000, preferably 0.01-600 mg/day. Spleen cells from mice immunised with Fast expressing COS cells
                                                                                                                                                  Sequence
                                                               91 hysspytf 98
                                                                                                Local Similarity 62.5% es 5; Conservative
                                                8 RYTGPYTF
                                                                                                                                                  105 AA;
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***** (MT)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:50:33 1999; MasPar time 4.35 Seconds 138.311 Million cell updates/sec

Tabular output not generated.

Title: Description: Perfect Score: Sequence: >US-08-991-628-6 (1-15) from US08991628.pep 109 1 SARTLNNRYTGPYTF 15

Scoring table: PAM 150 Gap 15

Searched: 122810 segs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 26.619; Variance 37.654; scale 0.707

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

221 221 232 232 233	Result
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50.60 50.60 55.60 55.60 55.60 55.60 55.60 55.60 55.60 55.60 56.60 56.60 56.60 56.60 56.60 56.60 56.60 56.60 56.60 56.60 56.60	% Query Match
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desmoglein 3 precurso mitochondrial import cellodextrin phosphor C28A5.4 protein (clon baseplate protein sp8 hypothetical protein hypothetical protein hypothetical protein probable N-acetyl-gam ferric exochelin bios hypothetical protein nitrate reductase gam nitrogenase (EC 1.18. RNA-directed RNA poly retrovirus-related po hypothetical protein transcription factor chicil synthase (EC 2 gamma A protein - Poa isocitrate dehydrogen alpha-amylase (EC 2 retrovirus-related po hypothetical protein	Description
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S38483 S38480 S38480 S38480 I49279 I49279 I49279 I49279 S33033 I49645 A05069 A050769 F64383 A050769 F64383 A26621 A266	3198	1196	1196	843	746	581	428	409	405	390	367	252	231	156	120	455	431	431	430	2115	1822	1317
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collagen alpha 2 chain collagen alpha 2 chain collagen alpha 2 chain collagen alpha 2 chain corticolloberin recept sauvagine/corticotrop CRF receptor mouse hypothetical protein polymerase polyprotein polymerase polyprotein polymerase polyprotein tobacco translation initiatio retrovirus related en hypothetical protein fol polyprotein alpha-ma pol polyprotein rad polyprotein appletion or at the collagen alpha a fibr collagen alpha 2 fibr collagen alpha 2 fibr	A43426	GNMVGV	GNMVRV	GNVWK	S44792	A42743	S36856	S12588	A69206	A26621	E64383	WMBV2P	S60769	A05069	I49645	S33033	149149	149279	A56726	S38480	S63985	A54831
	collagen alpha 2 fibr	•	•	•	•	•	glycolipid 2-alpha-ma	pol polyprotein – min	hypothetical protein	retrovirus-related en	translation initiatio	,		pol polyprotein - Rau	polymerase polyprotei		•	sauvagine/corticotrop	corticoliberin recept	nonstructural protein	collagen alpha 2 chai	nuclear pore complex

ALIGNMENTS

Query Match Best Local Sim Matches 15;	SUMMARY	937-966 110,180,545	515 540-55 540-999	52-157 160-267 270-383 390-495 496-598	1-23 24-49 50-999 50-615	#gene #COSS-references #map_position 18q12.1 CLASSIFICATION #superf KEYWORDS calcium transi	H (REFERENCE #authors #journal #title #cross-reference	RESULT 1 ENTRY TITLE ALTERNATE_NAMES ORGANISM DATE DATE
1 100.0%; Score 109; DB 1; Length 999; Similarity 100.0%; Pred. No. 6.01e-11; 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	#length 999 #molecular-weight 107502 #checksum 8311	#domain desmoglein repeat #label DG2\ #domain desmoglein repeat #label DG2\ #binding_site carbohydrate (Asn) (covalent) #status predicted	transmembrane #status predicted intracellular #status predicted desmortein repeat #label DGN	#domain cadherin repeat homology #label CR1\ #domain cadherin repeat homology #label CR3\ #domain cadherin repeat homology #label CR3\ #domain cadherin repeat homology #label CR4\ #domain cadherin repeat homology #label CR4\ #domain cadherin repeat homology #label CR4\	equence #status predicted #lade #status predicted #lade in homolog #status predicted	GDB:DSG3 iferences GDB:134030; OMIM:169615 iferences GDB:134030; OMIM:169615 iferences GDB:134030; OMIM:169615 #superfamily cadherin; cadherin repeat homology calcium binding; cell adhesion; duplication; glycoprotein; transmembrane protein	##molecule_type mRNA ##mesidues 1-999 ##label AMA ##cross-references GB:M76482; NID:g190751; PID:g190752 CS	#A1008 A41008 #authors A41008 #journal Cell (1991) 67.869-877 #title Autoantibodies against a novel epithelial cadherin in pemphigus vulgaris, a disease of cell adhesion. #cross-references MUD:92069753 #cross-references MUR8	IJHUG3 #type complete desmoglein 3 precursor - human pemphigus vulgaris antigen #formal_name Homo sapiens #common_name man 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 18-Sep-1998

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##residues 82-89;112-122;221-228;295-306;316-327;356-370 ##label
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Similarity 57.1%;
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Protein import into yeast mitochondria: the inner me import site protein ISP45 is the MPII gene product 335357
Kawaguchi, T.; Ikeuchi, Y.; Tsutsumi, N., N., J.; Arai, M.
J.; Arai, M.
J. Ferment. Bloeng. (1998) 85:144-149
Cloning, nucleotide sequence, and expression of the Clostridium thermocellum cellodextrin phosphorylax
                                                                                                                                                                                                                                                                                                                                                                                                                                     membrane protein; mitochondrion #length 431 #molecular-weight 48854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maarse, A.C.; Blom, J.; Grivell, L.A.; Meijer, EMBO J. (1992) 11:3619-3628
MPI1, an essential gene encoding a mitochondri protein, is possibly involved in protein imp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Saccharomyces cerevisiae) protein YI3299.09; protein YII022w
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12-Dec-1997
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                                                                                               cross-references MUID:90384864
                authors
                      ##cross-references EMBL:X15907; NID:g15321; PID:g15324
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##experimental_source ATCC 27405
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#length 980
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$C28A5,4 protein (clone C28A5) - Caenorhabditis elegans
#formal_name Caenorhabditis elegans
07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change
17-Oct-1997
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larity 60.0%;
Conservative
 submitted
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Efimov, V.P.; Prilipov, A.G.; Mesyanzhinov,
Nucleic Acids Res. (1990) 18:5313
Nucleotide sequences of bacteriophage T4 ger
                                                                                                                                                                                              #formal_name phage T4
host Escherichia coli
30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
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             Mesyanzhinov, V.V
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to JIPID,
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Pred. No. 1.36e+00;
2; Mismatches 3
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Best Local Similarity 53.8%;
Matches 7; Conservative
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##cross-references EMBL:AF077408; NID:g3319359; PID:g3319363
##experimental_source cultivar Columbia
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The order of association in the morphogenesis pathway is strictly determined except for gp 11 which can be added at any stage of the pathway. Gp 8 associates to the precursor structure after gp 7 binding and before gp 6 binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene 8 is directed clockwise in the T4 map; the . gene 8 overlaps with the 3'-end of gene 7 superfamily phage T4 baseplate protein gp8 baseplate; late protein specific that the protein specific specifi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harmon, G.; Langston, Y.; Stoneking, T.; Drone, submitted to the EMBL Data Library, July 1998 The sequence of Arabidopsis thaliana T7M24. T01862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.0%;
llarity 60.0%;
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85.20-86.20
                                                                                                                                                                                                                                                                                      #formal_name Mycobacterium tuberculosis
17-Jul-1998 #sequence_revision 17-Jul-1998
17-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                        B70854 #type complete
hypothetical protein Rv2991 - Mycobacterium
(strain H37RV)
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T7M24.4
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hypothetical protein T7M24.4 - Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouss
ole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barr III, C.E.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.;
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Pred. No. 2.07e+00
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Pred. No. 2.07e+00;
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Taylor, K.; Whitehead, S.; Barrell, B.G.
#journal Nature (1998) 393:537-544
#title Deciphering the biology of Mycobacterium tuberculosis
the complete genome sequence.
#cross-references_MUID:98295987
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#title
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##cross-references GB:AL021287; GB:AL123456; NID:g3261508;
PID:g2791588
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                                                                                                                                                                                                                                          ##experimental_source strain OT3
##note this accession replaces an interim accession for a
sequence replaced by GenBank
                                                                                                                                                                                                                                                                                                           ##molecule_type DNA
##residues 1-330 ##label KAW
##cross-references GB:AP000007; NID:g3236134; PID:d1031777; PID:g3258151
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3 RTLNNRYTGPYTF 15
                                           RGLNLRFTSDYNF
                                                                                                            h 54.1%;
Similarity 53.8%;
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Hino, Y.; Yamamoto, S.; Sekine, M.; Baba, S.; Kosugi, H.;
Hosoyama, A.; Nagai, Y.; Sakai, M.; Ogura, K.; Otsuka, R.;
Nakazawa, H.; Takamiya, M.; Ohiku, Y.; Funahashi, T.;
Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
A.; Aoki, K.; Yoshizawa, T.; Nakamura, Y.; Robb, F.T.;
Horikoshi, K.; Masuchi, Y.; Shizuya, H.; Kikuchi, H.
DNA Res. (1998) 5:55-76
Complete sequence and gene organization of the genome of a
hyper-thermophilic archaebacterium, Pyrococcus horikoshii
O73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable N-acetyl-gamma-glutamyl-phosphate reductase -
Pyrococcus horikoshii
#formal_name Pyrococcus horikoshii
14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change
14-Aug-1998
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#length 163 #molecular-weight 18204
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translation not shown
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Pred. No. 3.15e+00;
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Pred. No. 3.15e+00
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Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.;
Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short
J.M.; Olson, G.J.; Swanson, R.V.

#journal Nature (1998) 392:353-358
#title The complete genome of the hyperthermophilic bacterium
Aquifex aeolicus.
#cross-references MUID:98196666
#accession C70333
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#cross-references MUID:95191405
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                                                                                                                                                                                                                         ##residues 1-531 ##label AQF ##cross-references GB:AE000686; N
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                                                                                                                                                                                                                                                              ##molecule_type DNA
                                                                                                                                                                                                     ##experimental_source strain VF5
                                                                       / Match 54.1%;
Local Similarity 66.7%;
nes 8; Conservative
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                                     80 TLKNRLENPYTF 91
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4 TLNNRYTGPYTF
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phosphoribosylglycinamide formyltransferase homology
                                                                                                                                              aq_372
#length 531 #molecular-weight 62830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C70333 *type complete
hypothetical protein aq_372 - Aquifex aeolicus
*formal_name Aquifex aeolicus
08.May-1998 *sequence_revision 08-May-1998 *text_change
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Identification of genes involved in the sequestration of iron in mycobacteria: the ferric exochelin biosynthetic and
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homology #label PRGF
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Pred. No. 3.15e+00;
5; Mismatches 3
                                                                                        Score 59; DB 2; 1
Pred. No. 3.15e+00
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                                                                                                          Length 531;
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RESULT

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Lee, N.H.; Sutton, G.G.; Fleischmann, R.D.; Quackenbush, J.;
Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
Dougherty, B.A.; McKenny, K.; Adams, M.D.; Loftus, B.;
Peterson, S.; Reich, C.I.; McNeil, L.K.; Badger, J.H.;
Glodek, A.; Zhou, L.; Overbeek, T.; Cotton, M.D.; Weidman,
J.F.; McDonald, L.; Utterback, T.; Cotton, M.D.; Spriggs,
T.; Artiach, P.; Kaine, B.P.; Sykes, S.M.; Sadow, P.W.;
D'Andrea, K.P.; Bowman, C.; Fujii, C.; Garland, S.A.;
Mason, T.M.; Olsen, G.J.; Fraser, C.M.; Smith, H.O.; Woese,
C.R.; Venter, J.C.
C.R.; Venter, J.C.
Hjournal Nature (1997) 390:364-370
**Hitle sulfate-reducing archaeon Archaeoglobus fulgidus.
**cross-references MUID:98049343
**accession E69312
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Best Local Similarity 50.0%;
                                                                                                                                                                    #title Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional analysis and comparative genomics.
#cross-references MUID:98037514
#accession F69075
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##residues 1-332 ##label KLE
##residues GB:AE001069; GB:AE000782; NID:g2689392; PID:g2650124;
                                                                                                                                      ##status
##cross-references GB:AE000916; GB:AE000666; NID:g2622674; PID:g2622685
##experimental_source strain Delta H
                                                                                ##molecule_type_DNA
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J. Bacteriol. (1997) 179:7135-7155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F69075 #type complete
nitrogenase (EC 1.18.6.1) molybdenum-iron protein alpha
- Methanobacterium thermoautotrophicum (strain Delta
#formal_name Methanobacterium thermoautotrophicum
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
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05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
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                                                        1-469 ##label MTH
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TITLE
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KEYWORDS duplication; r
FEATURE
1-118 #region d
122-239 #region d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #journal
                                                                                                                                                                                                                                                                                                                                                         ##molecule_type genomic RNA
##residues 1-118,'FH',125-770 ##label KO4
##experimental_source strain 7-2
##experimental_source strain 7-2
In the duplication in this protein results from a tandem duplication in the virus genome found in some, but not all, virus strains.
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##residues 1-118,120-770 ##label
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##residues 1-770 ##label KOZ
##residues 1-770 ##label KOZ
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#residues 122-770 ##label KO2
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                                                                                                       RTLNNRYTGPYT 14
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#formal_name barley stripe mosaic virus, BSMV
30-Sep-1993 #sequence_revision 30-Sep-1993 #t
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The complete nucleotide sequence of barley stripe mosaic virus RNA 3 and its variability.
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vanadium-iron protein alpha chain homology
GNFF42 #type complete
retrovirus-related pol polyprotein -
melanogaster) retrotransposon 412
                                    GNFF42
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larity 50.0%;
Conservative
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RNA-directed RNA polymerase (EC 2.7.7.48)
barley stripe mosaic virus (strain 4-2)
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homology #label VIA
yth 469 #molecular-weight 52866 #checksum 1591
                                                                                                                                                                                                                                                            #region duplication\
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Pred. No. 4.77e+00;
2; Mismatches 3
                                                                                                                                                                       Score 58; DB 2; I
Pred. No. 4.77e+00;
4; Mismatches 2
                                                                                                                                                                                                         Length 770
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                fruit fly (Drosophila
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Bayev, A.A.
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Best Local Similarity 42.9%;
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##molecule_type DNA
1-1
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*cross-references MUID:86274717
*accession D29349
                                                                                                                                                                                                                 #accession
                                                                                                                                                                                                                            #submission #description
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##residues 1-1237 ##label YUK
##cross-references GB:X04132; GB:X03733; NID:g8500;
##DI:g1335652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##note
                                                                                                                                                                   ##cross-references
                                                                                                                                                                                   ##residues
                                                                                                                                                                                                 ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##cross-references FlyBase:FBgn0000006
                              19 SRAFFNRYPNPYS 31
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 N
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 ARTLNNRYTGPYT
                                                          h 52.3%;
Similarity 46.2%;
6; Conservative
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submitted to
                                                                                                                  12R
#length 175
                                                                                                                                                                                                                                                                          S48546
S48545
                                                                                                                                                                                                                                                                                                      hypothetical protein L8167.12
#formal_name Saccharomyces cerevisiae
02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change
12-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yuki, S.; Inouye, S.; Ishimaru, S.; Seur. J. Biochem. (1986) 158:403-410 Nucleotide sequence characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #superfamily pol polyprotein
aspartic proteinase; hydrolase;
                                                                                                                                                                                                                                                                                                                                                                               s48546 #type complete
hypothetical protein YLR193c -
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31_Dec-1988 #sequence_revision 31-Dec-1988 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #product retropepsin #status predicted #label RTP\
#active_site Asp (shared with dimeric partner) #st
                                                                                                                                                                   1-175 ##label PAU
es EMBL:U14913; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    predicted
 14
                                                                                                                     #molecular-weight 20108
                                                                                                                                                                                                                             the EMBL Data Library, September 1994 of S. cerevisiae cosmid 8167.
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Pred. No. 4.77e+00;
5; Mismatches 3
                                                          Score 57; DB 2; I
Pred. No. 7.17e+00;
4; Mismatches 3
                                                                                                                                                                    NID:g544497; PID:g544509; MIPS:YLR193c
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Search completed: Fri Jun 11 Job time : 92 secs.

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MPsrch_pp protein · protein database search, using Smith-Waterman algorithm

Tabular output not generated Run on: Fri Jun 11 17:45:15 1999; MasPar time 2.45 Seconds 173.166 Million cell updates/sec

Title:

Sequence: Description: Perfect Score: >US-08-991-628-6 (1-15) from US08991628.pep 1 SARTLNNRYTGPYTF 15 109

Scoring table: PAM 150 Gap 15

77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Dalabase: swiss-prot37 1:swissprot

Statistics: Mean 27.195; Variance 33.825; scale 0.804

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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NITROGENASE MOLYBDENUM RETROVIRUS RELATED POL TRANSCRIPTION FACTOR G CHITIN SYNTHASE 2 (EC ISCCITRATE DEHYDROGENA NUCLEOPORIN NUP145 (NU GVPF/L PROTEIN ACTOR X CORTICOTROPIN RELEASIN ZINC CARBOXYPEPTIDASE PROBABLE SERINE/THREON RETROVIRUS RELATED POL 29 KD PROTEIN REC	DESMOGLEIN 3 PRECURSOR MITOCHONDRIAL IMPORT I TRANSCRIPTION FACTOR X PUTATIVE HOMEOBOX PROT BASEPLATE STRUCTURAL P ZINC CARROXYPEPTIDASE	Description
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RNA POLYMERASE BETA SU	RNA POLYMERASE BETA SU	CYTOCHROME P450 6B2 (E	FLAGELLAR HOOK-BASAL B	NUCLEASE C1 (EC 3.1.30	HYPOTHETICAL 25.4 KD P	HYPOTHETICAL PROTEIN M	POL POLYPROTEIN [CONTA	HYPOTHETICAL 83.6 KD P	POL POLYPROTEIN [CONTA	PROBABLE MANNOSYLTRANS	RETROVIRUS-RELATED POL	PROBABLE G PROTEIN-COU	PUTATIVE ATP-DEPENDENT	GALACTOSE-1-PHOSPHATE	POL POLYPROTEIN [CONTA						
1.36e+01	1.36e+01	1.36e+01	1.36e+01	1.36e+01	1.36e+01		8.85e+00	8.85e+00	8.85e+00		8.85e+00			8.85e+00	8.85e+00	8.85e+00	8.85e+00	8.85e+00	8.85e+00	8.85e+00	8.85e+00

	1. SG3_HUMAN STANDARD; PRT; 95 33926; 1-OCT-1993 (REL. 27, CREATED) 1-OCT-1993 (REL. 27, LAST SEQUENCE UPI 1-VOV-1997 (REL. 35, LAST ANNOTATION UESMOGLEIN 3 PRECURSOR (130 KD PEMPHIGU SOG). SG3. SG3. UKARYOTA; METAZOA; CHORDATA; VERTEBRAY UKARYOTA; A disease of cell adhesion.", ELL 67:869-877(1991). ELL 67:869-877(1991). 1- PUNCTION: COMPONENT OF INTERCELLULL INVOLVED IN THE INTERACTION OF PLAK, FILAMENTS MEDIATING CELL-CELL ADHES: - SUBCELLULAR LOCATION: TYPE I MEMBRE: - TISSUE SPECIFICITY: EPIDERMIS, TONG CARCINOMAS. 1- DOMAIN: CALCIUM MAY BE BOUND BY THE (POTENTIAL). 1- DISEASE: PEMPHIGUS VULGARIS (PV) INDISEASE: PEMPHIGUS VULGARIS (PV) INDIS
CCERTER	UENCE FROM N.A. LINE; 92069753. GAI M., KLAUS-KOVTUN V., STANLEY J.R.; GAI M., KLAUS-KOVTUN V., STANLEY J.R.; GAI M., KLAUS-KOVTUN V., STANLEY J.R.; toantibodies against a novel epithelial cadherin in garis, a disease of cell adhesion."; L 67:869-877(1991). EUNCTION. COMPONENT OF INTERCELLULAR DESMOSOME JUNC INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND
88888	INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND FILAMENTS MEDIATING CELL-CELL ADHESION. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL, OESCARGINGME
3888	CARCLINOMAS. DOMAIN: CALCIUM MAY BE BOUND BY THE (POTENTIAL).
នននន	DISEASE: PEMPHIGUS VULGARIS (PV) IS A POTENTIALLY: DISEASE IN WHICH EPIDERMAL BLISTERS OCCUR AS THE RIGHTS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AGAINST DSG3.
3888	SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BEL DESMOSOMAL SUBFAMILY.
388	entry is copyright. It is produced iss Institute of Bioinformatics and
888	pean Bioinformatics Institute. There a non-profit institutions as long as i
8888	lfied ties send a
222222	EMBL; M76482; G190752; PIR; A41068; IJHUG3. MIN; 169615; PROSITE; PS002237; CADHERIN; 3. PRAM; PF00028; cadherin; 4. HSSP; P09803; 1EDH.

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Q01852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE: 93010953.

MAARSE A.C., BLOM J., GRIVELL L.A., MEIJER M.;

"MPII, an essential gene encoding a mitochondrial
is possibly involved in protein import into yeast
EMBO J. 11:3619-3628(1992).
                                                                                                                             MEDLINE; 93345448.

HORST M., JENOE P., KRONIDOU N.G., BOLLIGER L., OPPLIGER SCHERER P., MANNING-KRIEG U., JASCUR T., SCHATZ G.;

"Protein import into yeast mitochondria: the inner membra site protein ISP45 is the MPII gene product.";
                                                                                                                                                                                                                                                                                                                              STRAIN-5288C / AB972:

BARRELL B.G., BADCOCK K., BANKIER A.T., BOWMAN S., BROWN D.,

CHURCHER C.M., CONNOR R., COPSEY T., DEAR S., DEVLIN K., FRASER

GENTLES S., HAMLYN N., HORSNELL T.S., HUNT S., JAGELS K., JONES

LOUIS E., LYE G., MOULE S., MOULE T., ODELL C., PEARSON D.,

RAJANDREAM M.A., RILES L., ROWLEY N., SKELTON J., SMITH V.,

WALSH S.V., WHITCHEAD S.;

WALSH S.V., WHITCHEAD S.;

SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE
PRECURSOR (MITOCHONDRIAL PROTEIN IMPORT PROTEIN
TIM44 OR MPI1 OR MIM44 OR ISP45 OR YIL022W.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA, FUNGI, ASCOMYCOTA; HEMIASCOMYCETES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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IMPORT MACHINERY PROTEIN
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INNER MEMBRANE.
IMPORT OF
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15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
TRANSCRIPTION FACTOR XGATA-6B (GATA BINDTWO GATA-6A OR GATA-6.
XENOPUS LAFTYTO
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-LIVER;
GOVE C.D., WALMSLEY M., NIJJAR S., BERTWISTLE D., GUILLE PARTINGTON G., BOMFORD A., PARTIENT R.;
SUBMITTED (OCT-1996) TO EMBL/CENBANK/DDBJ DATA BANKS.
-I- FUNCTION: ASSOCIATED WITH CARDIAC SPECIFICATION AND CARDIAC-SPECIFIC TRANSCRIPTION DURING EMBRYOGENESIS.
THE EXPRESSION OF CARDIAC MHC-ALPHA IN VIVO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSIT CHAIN
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EMBL; X67276; G3967; -.
EMBL; Z47047; G763324; -.
PIR; S25196; S25196.
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                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
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MITOCHONDRION; INNER MEMBRANE; TRANSPORT; PRO
TRANSLOCATION; TRANSIT PEPTIDE; ATP-BINDING.
           NUCLEAR PROTEIN
                                                                                                                                                                                                                                                                                                                                 between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MESOBATRACHIA; PIPOIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 SSRTLTARYRSQYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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SUBUNIT: FORMS PART OF THE RECEPTOR COMPLEX THAT CO LEAST 3 DIFFERENT PROTEINS (TIM17, TIM3, TIM44).
SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: NUCLEAR.
SIMILARITY: TO OTHER GATA-TYPE TRANSCRIPTION FACTORS
                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboratic sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SARTLNNRYTGPYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101
431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                    REGULATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                    ACTIVATOR;
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MITOCHONDRIAL IMPORT I
TRANSLOCASE SUBUNIT TI
ATP (POTENTIAL).
W; 002E0771 CRC32;
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1. No. 5.37e-02;
Mismatches 4;
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                                    DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391 AA
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Query Match Best Local S Matches 1

TRANSPORT;

INNER MEMBRANE

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Best Local Similarity
Matches 8; Conser
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Best Local :
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ZN_FING
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SEQUENCE
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P19062;
01-NOV-199
01-NOV-199
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CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
PHARNITINA: RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WORMPEP; C28A5.4; CE05325.
PROSITE; PS00027; HOMEOBOX_1;
PROSITE; PS50071; HOMEOBOX_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBMITTED (APR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE DISTAL-LESS FAMILY OF HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDAT
PUTATIVE HOMEOBOX PROTEIN C28A5.4.
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Q18273;
BACTERIOPHAGE T4.
VIRUSES; DSDNA VIRUSES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL PROTEIN; HOMEOBOX; DNA-BINDING; NUCLEAR PROTEIN DNA_BIND 102 161 HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                       BASEPLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 ARPLNGSYGSPYT
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les 6; Consei
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236
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293
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larity 61.5%;
Conservative
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260
79
245
298
41503
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PROTEIN GP8.
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GATA-TYPE.
POLY-SER.
POLY-THR.
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POLY-SER.
221DD428 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 60; I
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  STAGE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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    PHAGES; MYOVIRIDAE;
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METAL
                                                                       HYDROLASE;
                                                                                                                   PFAM; PF00246; Zn_carbOpept;
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Query Match
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Matches 6; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CBPZ_SIMVI
P42788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EFIMOV V.P., PRILIPOV A.G., MESYANZHINOV V.V.;
"Nucleotide sequences of bacteriophage T4 genes 6, 7
NUCLEIC ACIDS RES. 18:5313:5313(1990).
-I- FUNCTION: STRUCTURAL COMPONENT OF THE BASEPLATE.
                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                    use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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PROSITE; PS00132; CARBOXYPEPT PROSITE; PS00133; CARBOXYPEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
ZINC CARBOXYPEPTIDASE (EC 3.4.17.-) (FRAGMENT).
                                             EMBL; L08481;
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 94093864.
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ilarity 60.0%;
Conservative
                                             G161186;
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  CARBOXYPEPT_ZN_1;
CARBOXYPEPT_ZN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARTHROPODA;
NEMATOCERA;
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Pred. No. 5.92e-01;
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ALDREDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,
ALDREDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,
ALDREDGE T., BASHIRZADEH R., ECON R., COOK R., GILBERT K.,
ALDREDGE T., BASHIRZADEH R., WANG Y., WIERZBOWSKI J., GIBSON R.,
ANDRIANI N., CARUSO A., BUSH D., SAFER H., PANWELL D., PRABHAKAR S.,
ALDREDGE G., GOYAL A., PIETROVSKI J., GIBSON R.,
ALDREDGE C., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
ALDRIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
COMPLETE GENOME SEQUENCE OF MECHANOBACTERIUM THERMOMETOPHICUM
AND ANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
COMPLETE GENOME SEQUENCE OF MECHANOBACTERIUM THERMOMETOPHICUM
AND ANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
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AND ANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
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COMPLETED BY THE MITTROGENASE COMPLEX, WHICH HAS 2 COMPONENTS: THE
COMPLETE GENOME SECUENCE OF THE MOLYBDENUM-IRON PROTEIN
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C. I. SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS THAT BINDS
C. JONIDIZED FERREDOXIN + 2 NH(3) + N ADP + N ORTHOPHOSPHATE.
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                                                                                                                                                                                          SEQUENCE 469
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SMITH D.R., DOUCETTE-STAMM L.A.,
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ARCHAEA; EURYARCHAEOTA; METHANOBACTERIALES; METHANOBACTERIACEAB;
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15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NITROGENASE MOLYBDENUM-IRON PROTEIN ALPHA CHAIN
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L. No. 9.43e-01;
Mismatches 5
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                                                    1.49e+00;
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01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
RETROVIRUS-RELATED POL POLYPROTEIN FROM TRANSPOSON 412 [CONTAINS: ENDONUCLEASE].
                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
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POSOPHILA MELANOGASTER (FRUIT FLY).

EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA;

PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPH!
                                                                                                                                                                                                                        GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
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FLYBASE; FB9N000006; 412.
PROSITE; PS00141; ASP_PROTEASE;
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BURCH J.B.E., EVANS T.; "GATA-4/5/6, a subfamily of three transcription factors transcribed in developing heart and gut."; J. BIOL. CHEM. 269:23177-23184(1994).
                                                                                        MEDLINE; 94365018.
LAVERRIERE A.C., MACNEILL C.,
                                                                                                                                                                                                                                                                                                                                                                                                                               GAT6_CHICK P43693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleotide sequence characterization of a Drosophila retrotransposon, 412.";
EUR. J. BIOCHEM. 158:403-410(1986).
-I- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY U22.
                                                                                                                                               STRAIN-WHITE LEGHORN;
                                                                                                                                                                            SEQUENCE FROM N.A.
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YUKI S., INOUYE S.,
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Similarity 42.9%;
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                                                                                                MUELLER C.,
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of a Drosophila
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A; EPHYDROIDEA;
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01-CCT-1996 (REL. 34, I
01-CCT-1996 (REL. 34, I
01-CCT-1996 (REL. 34, I
CHITIN SYNTHASE 2 (EC
TRANSFERASE 2).
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P30584;
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                        modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                            PROC.
                                                                                                                                                                                                                                     BOWEN A.R., CHEN-WU J.L., ROBBINS P.W.;
                                                                                                                                                                                                                                                                                                                            STRAIN-FGSC 89;
                                                                                                                                                                                                                                                                                                                                                                                   EMERICELLA NIDULANS
EUKARYOTA; FUNGI; AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U11889; G511484; -. PROSITE; PS00344; GATA_ZN_FINGER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SUBCELLULAR LOCATION: NUCLEAR.
-i- TISSUE SPECIFICITY: MOUNDANT IN STOMACH, AND IN SMALL INTESTINE. LOWER LEVELS IN LUNG, LIVER, OVARY AND HEART.
-i- SIMILARITY: TO OTHER GATA-TYPE TRANSCRIPTION FACTORS.
                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                                    SUBMITTED (NOV-1993) TO EMBL/GENBANK/DDBJ DATA
                                                                                                                                                                                                                                                                                                                                                                     EUROTIALES;
                                                                                                                                                                                                                                                                                                                                                                                                              CHS2 OR CHSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRANSCRIPTION REGULATION;
                                                                                                                                                                                                                                                                          SEQUENCE OF 303-491 FROM N.A.
                                                                                                                                                                                                                                                                                                                   KOJIMA N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
                                                                                                                             SUBCELLULAR LOCATION: PLASMA MEMBRANE-BOUND. SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY.
                                                                                                                                                        GLUCOSAMINYL) ] (N+1)
                                                                                                                                                                     BETA-D-GLUCOSAMINYL)](N) = UDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARTLNNRYTGPYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRPLNGSYPAPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00320
P17678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN.
                                                                                                                                                                                                                                                               92115692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
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240
387
                                                                                                                                                                                                                                                                                                                                                                     TRICHOCOMACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.3%;
larity 46.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                 NS (ASPERGILLUS NIDULANS).
ASCOMYCOTA; EUASCOMYCETES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205
259
244
40249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14
                                                                                                                                                                                                                                                                                                                                                                                                                              CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
2.4.1.16) (CHITIN-UDP ACETYL-GLUCOSAMINYL
                                                                                                                                                                                                                                                 MOMANY M., YOUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIVATOR; DNA-BINDING; ZINC-FINGER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 57; DB 1; 1
Pred. No. 2.35e+00,
3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATA-TYPE.
GATA-TYPE.
GATA-TYPE.
POLY-THR.
6E67EA1C CRC32;
                                                                                                                                                                                                                                                                                                                                                                     EMERICELLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                       +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1013 AA.
                                                                                                                                                                      [1,4-(N-ACETYL-BETA-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                            There are no rest
                                    . Usage by and for http://www.isb-sib
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                                                 Usage
                                                                                                                                                                                 BIOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 387;
                                                                                                                                                                                                                                                                                                     BANKS
                                                                                                                                                                                                                                                  SZANISZLO P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                 ,4-(N-ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a collaboration - MRL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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G465390;

between the Swiss Institute of Bioinformathe European Bioinformathos Institute. The use by non-profit institutions as long modified and this statement is not removed

ormatics and the EMBL outst There are no restrictions ong as its content is in

through

a collaboration

outstation

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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDH1_YEAST
P28834;
01-DEC-1992
01-JUL-1993
01-NOV-1997
                                                                                                                                                                                                                                                      MEDIINE, 90330530.
MEDIINE, 90330530.
MEDIINE, 90330530.
KEYS D.A., MCALISTER-HENN L.;
"Subunit structure, expression, and function of NAD(H)-specific socitrate dehydrogenase in Saccharomyces cerevisiae.";
I. BACTERIOL, 172:4280-4287(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MULTIGENE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M82939; G168041; -.
PIR; C45188; C45188.
TRANSFERASE; GLYCOSYLTRANSFERASE; TRANSMEMBRANE; CELL WALL;
                                                                                                                             SEQUENCE FROM N.A.

DUESTERHOEFT A., FLOETH
HILBERT H., MOESTL D.;
SUBMITTED (MAY-1996) TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISOCITRATE DEHYDROGENASE (NAD), MITOCHON (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) IDH1 OR YNLD37C OR N259C, SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)
                                                                                  INCLUDING AMP, NAD+, AND CITRATE.
-!- SUBUNIT: OCTAMER OF TWO NONIDENTICAL SUBUNITS
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
                                                                                                                                                                                                                  GRIVELL L.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                             of NAD(+)-dependent isocitrate dehydrogenase cerevisiae.";
                                                                                                                   -1- ENZYME REGULATION: ALLOSTERICALLY REGULATED
                                                                                                                                                                                                        "Yeast mitochondrial NAD(+)-dependent isocitrate dehydrogenase is
                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                                                    RNA-BINDING
                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 12-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; FUNGI; ASCOMYCOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                   . BIOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 ARTAESRYPERYSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N
                                                               SIMILARITY: BELONGS TO THE ISOCITRATE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARTINNRYTGPYTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                        94089379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MCALISTER-HENN L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REL. 24, CREATED)
(REL. 26, LAST SEQUENCE UPDATE)
(REL. 35, LAST ANNOTATION UPDATE)
(REL. 35, LAST ANNOTATION UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
(REL. 37, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  267:16417-16423(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                            BEDNARZ A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
2
2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                              TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113678
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X
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                  FRITZ C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                             VAN OOSTERUM K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEMIASCOMYCETES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene encoding the IDH1 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360
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2.35e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NDRIAL SUBUNIT 1 PRECURSOR (NAD+-SPECIFIC ICDH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC32;
                                                                          AND ISOPROPYLMALATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                         from Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SACCHAROMYCETALES
                                                                                                                                                                                                                              DEKKER P.J
                                                                                                                     ВХ
                                                                                              IDH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325-333 AND 339-356
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                                                                                                                     SEVERAL
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Best Local
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDIJNE; 94320139.

FABRE E., BOELENS W.C., WIMM
"Nup145p is required for nuc
homopolymeric RNA in vitro v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N145_YEAST
P49687;
P49687;
O1-FEB-1996
O1-FEB-1996
O1-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M95203; G171766; ...
EMBL; Z71313; E239881; ...
PIR; S31264; S31264.
SGD; L0000840. ...
                                                                                                                                                                                                                             MEDLINE; 94253246.

WENTE S.R., BLOBEL G.;

WENTE S.R., BLOBEL G.;

"NUP145 encodes a novel yeast glycine-leucine-phenylalanine-glycine

"GLFG) nucleoporin required for nuclear envelope structure.";

J. CELL BIOL. 125:955-969(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
NUCLEOPORIN NUP145 (NUCLEAR PORE PROTEIN NUP145
NUP145 OR YGLO92W.
SACCHAROWCES (CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                      between
the Euro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OXIDOREQUCTASE; NAD; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; ALLOSTERIC ENZIME; RNA-BINDING. TRANSIT 1 11 MITOCHONDRION.
                                                                                              YEAST 13:1077-1090(1997).

-I- FUNCTION: MAY PLAY A DIRECT ROLE IN ROLE IN PROTEIN IMPORT. BIN IN SUBCELLULAR LOCATION: NUCLEAR PORE IN DOMAIN: CONTAINS G-L-F-G REPEATS.
                                                                                                                                                             "Sequence analysis of chromosome VII.";
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-ATCC 26109 / X2180;
MEDLINE; 94253246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
              modified
                                                                                                                                                                                                     STRAIN-S288C;
MEDLINE; 97435481
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 AERTLPKKYGGRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \vdash
                    SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                      SIMILARITY: BELONGS TO THE GLFG FAMILY OF NUCLEOPORINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L0000849; IDH1.
ITE; PS00470; IDH_IMDH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SARTLNNRYTGPYT
                                                                                                                                                                                                                                                                                                                                                          78:275-289(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00180; isodh; 1.
P00351; iosi.
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             non-profit institu
and this statement
                                                                                                                                                                                          BRUECKNER M.,
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360
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larity 42.9%;
Conservative
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39324
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                                                                                                                                                                              203
                                                                                                                                                                                                                                                                                                                                                                      , WIMMER C.,
or nuclear ex
itro via a no
                                                                                                                                                                             SCHAEFER M., MUELLER-AUER kilobases from Saccharom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 56;
Pred. No.
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            is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISOCITEATE DEHYDROGENASE [NAD],
MITOCHONDRIAL SUBUNIT 1.
BINDING TO ISOCITEATE (BY SIMIL)
7D6BCA76 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                             ROLE IN NUCLEOCYTOPLASMIC ORT. BINDS HOMOPOLYMERIC REAR PORE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                     c export of mRNA a novel conserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN NUP145).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 1; L
3.68e+00;
                                                                                                                                                                            ELLER-AUER S.;
Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 360
                                                                                                                                                                                                                                                                                                                                                                     , HURT E.C.;
A and binds
ed motif.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SACCHAROMYCETALES;
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                                                                                                                                                                             cerevisiae
                                                                                                                             RNA
                                                                                                                                        EXPORT
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Best Local S
Matches
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Best Local
                                                                                                                                                                                                                                                                                             MEDLINE: 97217685.

KINSMAN R., HAYES P.K.;

"Genes encoding proteins he
f L are located downstream
flos-aquae.";

DNA SEQ. 7:97-106(1997).
-i- FUNCTION: MAY PLAY A S'
VESICLE SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X7
EMBL; Z3
EMBL; Z7
SGD; L00
NUCLEAR
                           Y4ZC_RHISN
P55730;
01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996
01-OCT-1996
15-JUL-1998
                                                                                                                                                                               EMBL; U17
GAS VESIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a celebrate the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1145 NAQALKDRYEGNY
                  HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CCAP 1403/13F;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                     ANABAENA FLOS-AQUAE.
BACTERIA; CYANOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  GVPF/L PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVPL_ANAFL
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                                                                                                                         228 RIRYNNFTAPYTF
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; Z32672;
; Z72614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SARTLNNRYTGPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L0001294; NUP145
                                                                                                      RTLNNRYTGPYTF
                                                                                                                                                                                                  U17109; G595974; -.
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CT 281 282
CT 1142 1142
CT 1310 1317
                                                                                                                                         h 50.5%;
Similarity 53.8%;
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (REL. 34, CREATED)
(REL. 34, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
                 (REL. 35, CREATED)
(REL. 35, LAST SEQUENCE UP
(REL. 35, LAST ANNOTATION
2 28.3 KD PROTEIN Y4ZC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G505271; -.; G496731; -.; E243975; -.
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                                                                 STANDARD;
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                                                                                                                                         Score 55; D
Pred. No. 5.
2; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WW.
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Pred.
5; N
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NA -> QR (IN REF. 2).
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LMKCTYKI -> FEVYI (IN
                                                                 PRT;
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                                     UPDATE)
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5.72e+00;
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RHIZOBIUM SP.

(STRAIN NGR234).

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Query Match 50.5%;
Best Local Similarity 60.0%;
Matches 6; Conservative
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Q91678;
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
TRANSCRIPTION FACTOR XGATA-6A (GATA BINDING FACTOR-6A).
GATA-6A OR GATA-6.
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000109; G2182749; -.
HYPOTHETICAL PROTEIN; PLASMID.
SEQUENCE 261 AA; 28349 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 97305956.
FREIBERG C.A., FELLAY R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLASMID SYM PNGR234A.
BACTERIA; PROTEOBACTERIA;
RHIZOBIACEAE; RHIZOBIUM.
[1]
                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         "The Xenopus GATA-4/5/6 genes are associated with cardiac specification and can regulate cardiac-specific transcription during embryogenesis.";
DEV. BIOL. 174:258-270(1996).
-I- FUNCTION: ASSOCIATED WITH CARDIAC SPECIFICATION AND CAN REGULATE CARDIAC-SPECIFIC TRANSCRIPTION DURING EMBRYOGENESIS. ACTIVATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular basis of symbiosis between Rhizobium and legumes.", NATURE 387:394-401(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-HEART, AND GUT;
MEDLINE; 96175597.
JIANG Y., EVANS T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PERRET X.
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|:| |||: |
3 RTLNNRYTGP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MESOBATRACHIA; PIPOIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: TO P.SYRINGAE (PV. PHASEOLICOLA) AVIRULENCE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVRPPH3
                                                                                                                                                                                             DEVELOPMENTAL STAGE: EXPRESSED IN CARDIAC PROGENITORS DURING EMBRYOGENESIS AND UPREGULATED DURING GASTRULATION. SIMILARITY: TO OTHER GATA-TYPE TRANSCRIPTION FACTORS.
                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: EXPRESSED INTESTINE, AND STOMACH. FOUND AND COLON.
                                                                                                                                                                                                                                                                                                                                  THE EXPRESSION OF CARDIAC MHC-ALPHA IN VIVO. SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA; PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAIROCH A., BROUGHTON W.J., ROSENTHAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 55; DB 1; I
Pred. No. 5.72e+00;
2; Mismatches 2
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                                                                                                                                                                                                                                                                                      AT HIGH LEVELS IN HEART, AT LOWER LEVELS IN LUNG,
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SQ SQ
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                 В
                                 Query Match
Best Local Similarity
Matches 7; Conser
                                                                              NUCLEAR PROTEIN.
ZN_FING 182
ZN_FING 236
DOMAIN 293
                                                                                                                         EMBL; U45454; G1209880; -.

PROSITE; PS00344; GATA_ZN_FINGER;

PFAM; PF00320; GATA; 2.

HSSP; P17678; 1GAU.
                                                                      SEQUENCE
                                                                                                                   TRANSCRIPTION REGULATION;
                 120 ARSLNGSYGSHYT 132
2 ARTLNNRYTGPYT
                                                                     236
293
391 AA;
                                    Conservative
                                                                               206
260
298
                                            50.5%;
                                                                      41780
                                                                      MW;
                                                                                                                   ACTIVATOR; DNA-BINDING; ZINC-FINGER;
                                          Score 55; D
Pred. No. 5.
                                                                               GATA-TYPE.
POLY-SER.
                                    2
                                                                                                 GATA-TYPE
                                                                      1BC6C528 CRC32;
                                     Mismatches
                                     DB 1,
5.72e+00;
                                                     Length 391;
                                     Indels
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SOURCE COCCOCCE RESERVED OCC

Search completed: Fri Jun 11 17:45:23 1999 Job time : 8 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:40:44 1999; MasPar time 6.10 Seconds 134.150 Million cell updates/sec

Tabular output not generated.

Sequence: Description: Perfect Score: Title: >US-08-991-628-6 (1-15) from US08991628.pep 109 SARTLNNRYTGPYTF 15

Scoring table: PAM 150 Gap 15

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb19

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 26.176; Variance 36.644; scale 0.714

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2098 75554 3221 112 113 115 115 115 115 115 115 115 115 115	Result No.
55 57 77 78 88 88 88 88 88 88 88 88 88 88 88	Score
556.0 566.0 566.0	Query Match I
993 11 980 12 973 10 973 10 973 10 330 330 330 330 330 330 330 330 330 33	Length DB
2024780 2024780 2024780 2024780 2024780 2024780 2024780 2025339 202539 2025339	ij
	Des
DESMOGLEIN 3 (FRA POL POLYPROTEIN (CELLODEXTRIN PHOS CELLODEXTRIN PHOS T7M24.4 FROTEIN. 18.2 330AA LONG HYPOTH FERRIC EXOCHELIN 130AA LONG HYPOTH FERRIC EXOCHELIN 14 FROTEIN VP1 COAT PROTEIN VP1 NITRATE REDUCTASE CE-FKH-1. 14 FYPOTHETICAL 87.2 ENVELOPE GLYCOPRO SIMILAR TO MYST1 P CODED FOR BY C. E CCP. INTEGRASE (FRAGME	Description
DESMOGLEIN 3 (FRAGMENT POCL POLYPROTEIN (FRAGMENT POLYPROTEIN (FRAGMENT POLYPROTEIN PROSPHORY IT M24.4 PROTEIN. HYPOTHETICAL 18.2 KD P 330AA LONG HYPOTHETICAL 62.8 KD P 20AT PROTEIN VP1 (FRAGMITRATE REDUCTASE, GAMMITRATE REDUCTASE, GAMMITRATE GLYCLOPROTEIN SIMPLIAR TO MSF1 PROTEI CODED FOR BY C. ELEGAN CCP. INTEGRASE (FRAGMENT). INTEGRASE (FRAGMENT). INTEGRASE (FRAGMENT). INTEGRASE (FRAGMENT).	
HEN DENDE DE HE	Pred.
9.29e-02 1.35e+00 1.35e+00 2.09e+00 3.20e+00 3.20e+00 3.20e+00 4.88e+00 4.88e+00 4.88e+00 7.42e+00 7.42e+00 7.42e+00 7.42e+01 1.12e+01 1.12e+01	No.

45	44	43	42	41	40	3 9	38	37	36	35	34	ယ	32	31	30	29	28	27	26	25	24	23	22	21
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075592	039735	Q83362	092808	P70355	041250	Q83398	Q39392	Q61530	010624	Q83367	Q83376	Q61870	Q96797	074872	082468	Q86500	Q26638	P70248	Q80873	Q80875	Q60051	202474	042886	000414
PROTEIN ASSOCIATED WIT	GAG-POL POLYPROTEIN (P	GAG-POL POLYPROTEIN.	PR180.	GAG-POL POLYPROTEIN.	COMPLETE GENOME (FRAGM	REVERSE TRANSCRIPTASE.	SRK29 PROTEIN KINASE.	INTEGRASE (FRAGMENT).	INTEGRASE (FRAGMENT).	REVERSE TRANSCRIPTASE	REVERSE TRANSCRIPTASE	POL PROTEIN (FRAGMENT)	POL POLYPROTEIN PRECUR	HYPOTHETICAL 52.6 KD P	PROTEIN PHOSPHATASE-2C	M33 RNA FOR A NONSTRUC	2 ALPHA FIBRILLAR COLL	MYOSIN IF.	HYPOTHETICAL 87.3 KD P	HYPOTHETICAL 74.0 KD P	ALPHA-AMYLASE PRECURSO	PUTATIVE RNA-DIRECTED	HYPOTHETICAL 14.9 KD P	ORF DERIVED FROM D1 LE
2.52e+0	٠	٠	'n			٠	٠	•	٠	٠	•	•	•		•	1.12e+01	٠	1.12e+01	٠	1.12e+01	1.12e+01		1.12e+01	1.12e+01

888		RES	Qy Db	3. M O	SQ	K.	D DR	묽	3 2	RA	R R	2 8	8	လ	S D	DT.	3 5	AC	RES
FÜĞÜ RUBRIPES (JĀPANESE PUFFERFISH) (TAKIFUĞU RUBRIPES). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYĞII; NEOPTERYĞII; TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYĞII; PERCOMORPHA;	01-NOV-1998 (TREMBLREL. 08, CREATED) 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) POL. POLYPROTEIN (FRAGMENT).	RESULT 2 ID 093284 PRELIMINARY; PRT; 1187 AA. AC 093284:	512 SVRTLDRGKYTGDYT 526 : : 1 SARTLN-NRYTGPYT 14	Query Match 61.5%; Score 67; DB 11; Length 993; Best Local Similarity 66.7%; Pred. No. 9.29e-02; Matches 10; Conservative 2; Mismatches 2; Indels 1; Gaps 1;	NOW_TER 993 993 SEQUENCE 993 AA; 107888 MW; 881794BD CRC32;	HESION;	PROSITE; PS00232; CADHERIN; 2.	TER T MEMBERSHAP FROM THE	SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.		SEQUENCE FROM N.A. STRAIN-BALB/C:	SCIUROGNATHI; MURIDAE; MURINAE; MUS.	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;	MUS MUSCULUS (MOUSE).	DESMOGLEIN 3 (FRAGMENT). DSG3.	1-NOV-1998 (TREMBLREL: 08, LAST ANNOTATIO	01-JAN-1998 (TREMBLREL, 05, CREATED)		RESULT 1 ID 035902 PRELIMINARY; PRT; 993 AA.

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RESULT OF A COLOR OF THE SECOND OF THE SECON
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ANDOLINE; 9731267.

ANDOLINE; 97312
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Best Local :
           Matches
                                                 Query Match
Best Local
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005776
005776;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIRARD M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MURPHY E., KORBER B.T., GEORGES-COURBOT M.C., YOU B., PINTER A., COOK D., KIENY M.P., GEORGES A., MATHIOT C., BARRE-SINOUSSI F.,
                                                                                                                                                   SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS EMBL; U14913; G544509; -. SEQUENCE 175 AA; 20108 MW; 9FCA0042 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-S288C (AB972);
PAULEY A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILAR TO MSF1 PROTEIN.
L8167.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENVELOPE PROTEIN.
                                                                                                                                                                                                                                                             STRAIN-S288C (AB972);
CHERRY J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-S288C (AB972);
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             SUBMITTED (SEP-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-S288C (AB972);
WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBMITTED (SEP-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
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nes 7; Conservative
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| |||:||:
6 NNRYTGPYTF 15
   Match 52.3%;
Local Similarity 46.2%;
les 6; Conservative
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Pred. No. 7.42e+00;
2; Mismatches 1
Score 57; DB 3; Length 175; 
Pred. No. 7.42e+00; 
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15E98296 CRC32;
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19 SRAFFNRYPNPYS 31

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0y 2 ARTLNNRYTGPYT 14
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Search completed: Fri Jun 11 17:42:47 1999 Job time : 123 secs.

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(ME)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:52:50 1999; MasPar time 4.77 Seconds
Tabular output not generated. 66.862 Million cell updates/sec

Title: >US-08-991-628-7
Description: (1-15) from US08991628.pep
Perfect Score: 99
Sequence: 1 QSGTMRTRHSTGGTN 15

Scoring table: PAM 150
Gap 15

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part23
24:part24 25:part25 36:part26 27:part27 28:part23
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 17.125; Variance 54.917; scale 0.312

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

11111111111111111111111111111111111111	Result
00004444444444444444000000000000000000	Score
100.0 10	Query Match
15 999 572 140 802 830 987 1106 1130 1130 1130 1130 1130 1207 483	Length
20 50 11 11 11 11 11 11 11 11 11 11 11 11 11	BB
W04847 R30742 R06023 R10423 R10423 R10423 R56550 W80314 W57056 W80312 W877056 W80313 R7245 W80313 W80313 R7455 W80311	IB
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either an isolated human non-collagen or non-myslin basic protein (MBP) polypeptide which is capable of tolerising an individual to an autoantigen; or an isolated human pathogen polypeptide capable of polypeptide (whether self or non-self) includes in both cases, the polypeptide (whether self or non-self) includes an amino acid sequence corresponding to a sequence motif for a MHC class II protein, such as HLA-DR, which is associated with a human autoimmune disease and which binds to the polypeptide to activate autoreactive derived from the human desmoglein 3 protein (amino acids 762-786) and is implicated as a self epitope in pemphigus vulgaris. Peptides derived from the-human desmoglein protein are described in w04841-47.	WO9627387-A1. 12-SEP-1996; U03182. 07-MAR-1995; US-400796. (HARD) HARVARD COLLEGE. Strominger JL, Wucherpfennig KW; WPI; 96-425218/42. Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens - useful in disease treatment, and method for identification of other self and non-self antigens implicated in auto-immune disease Claim 1; Page 42; 58pp; English.	M04847 standard; peptide; 15 AA. W04847; W04847; 18-FEB-1997 (first entry) Self epitope of desmoglein 3, implicated in autoimmune disease. Tolerisation; self-epitope; antigen; autoimmune disease. autoantigen; HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris; desmoglein; multiple sclerosis; herpes simplex virus; adenovirus; phosphomannomutase; human papillomavirus; Epstein-Barr virus; DNA polymerase; influenza; haemagglutinin; reovirus; sigma protein. Homo sapiens.

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R30742;
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15-DEC-1992.
27-NOV-1991; 798918.
27-NOV-1991; US-798918.
(USSH) US DEFT HEALTH & HUM
AMBGBA M, Klaus-Kovtun V,
WPI; 93-067436/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding pemphigus vulgaris antigen - useful in proteins for diagnostic and therapeutic uses Disclosure; Fig 7; SOpp; English.
This sequence is the pemphigus vulgaris 130kD antigen. The protein and its encoding DNA may be used in the diagnosis and treatment of pemphigus vulgaris. It is thought that the antigen may be a cell adhesion molecule.
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Human pemphigus vulgaris 130kD antigen.
Pemphigus vulgaris; skin disease; autoantibodies;
keratinocyte cell surface antigen; glycoprotein; cell adhesion.
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Haemagglutinin neuraminidase; vaccim
Rovine parainfluenza type III virus.
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N-PSDB; Q35992.
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                                                                                                                                                                                                                                                                       Recombinant vaccinia virus - is which all or part of DNA coding membrane fusion protein in combined to genom region.

Disclosure; p; Japanese.

Fragment of parainfluenza viral membrane fusion protein encoding may be incorporated into the vaccina virus, which may then be use as a live vaccine for cows.

Sequence 572 AA;
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09-DEC-1988; JP-311655.
(JAPG ) NIPPON ZEON KK.
WPI; 90-228484/30.
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702156883-A.
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Pred. No. 5.56e-04;
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4; M
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Matches 6; Conser
                                                                        Query Match
Best Local Similarity
Matches 8; Conser
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21-JAN-1993; US-007107.
(UYFL) UNIV FLORIDA.
GUY CL, Haskell DW, Ho
WPI; 94-264100/32.
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24-JUL-1987; US-077561.
(STACZ) STACEY G. SCHOLL MG, Nieuwkoop AJ, Deshmane NA, Banfalvi WPI; 91-036225/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e.g. plant parasite toxin bisclosure; Page 4; Hipp; English. The nod L gene product may be used to Nod- mutants of Bradyrhizoblum enhance nodulating ability.

Sequence 140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; Q10325.

Nod genes and control sequences of used for improving nodulation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nod L gene product.
Nod genes; parasite; toxin;
Bradyrhizobium japonicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R10423 standard; Protein; 140
                                                                                                                                   transformation

Claim 6; Page 29; 49pp; English.

Claim 6; Page 29; 49pp; English.

Transgenic plants expressing this cold acclimatization

protein have improved cold tolerance and/or drought-resistance.

The cell expressing the protein is from the family Solanaceae,

a citrus plant, a bacterium or a yeast cell.

Sequence 802 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US4983519-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-APR-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cold acclimatization protein CAP160 from spinach leaf. Cold acclimatization; cold-tolerance; transgenic plant; drought-resistance; drought-tolerance; crop improvement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JAN-1991
                                                                                                                                                                                                                                                                                         Cold acclimatisation proteins CAP85 and CAP160 and their nucleotide sequences - used to confer increased cold tolerance and drought resistance on plants and microorganisms by genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spinacia oleracea.
WO9417186-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R56550;
20-FEB-1995
                                                                                                                                                                                                                                                                                                                                                         N-PSDB; Q70904.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-AUG-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    freezing-tolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R56550 standard; Protein;
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4 TMRTRHSTGGTN 15
                        qdtgtrtrhitqgte
QSGTMRTRHSTGGTN
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                                                                            Conservative
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                                                                                            48.5%;
                                     782
15
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Pred. No.
5; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter; nodulation; flavones; nod L.
                                                                          Score 48; DB 11;
Pred. No. 2.29e+02;
1; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used to restore nodulating ability bium or Rhizobium strains and can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                re 49; DB 2; Le
d. No. 1.82e+02;
Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                Neven LG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 140;
                                                                                                                     Length 802
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RESULTATION OF COLUMN AND COLUMN 
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The present sequence represents type IV CIITA (class II transactivator) protein. The products can be used to treat diseases for which cenhanced expression of genes coding for MHC class II molecules is desired, especially where the enhanced expression is desired in dendritic cells or after induction by a cytokine, especially can be used to treat diseases for which reduced expression of genes coding for MHC class II molecules is desired for dendritic cells or after induction by a cytokine, especially can be used to treat diseases for which reduced expression of genes coding for MHC class II molecules is desired or can be used as vaccines, especially for cancer treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches
                                                                                                                                                                                                                                          08-OCT-1997; G02751.
21-MAR-1997; GB-005911.
08-OCT-1996; GB-020940.
(CHIL-) INST CHILD HEALTH.
Fabre JW, Gustafsson KT, Yul
rejection
Claim 15; Pages 69-72; 104pp; English.
This represents a 151 deletion mutant,
(CIITA) polypeptide. The N-terminal re
                                                                                         N-PSDB; V28717.

Deleted form of the class II trans-activator that reduces class II antigen expression - and ribozyme directed to trans-activator mRNA, related nucleic acid, vectors, transformed cells and antibodies, used for treating auto-immune disease and to inhibit xeno-graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1999 (first entry)
CIITA (class II transactivator) type IV protein.
CIITA gene; class II transactivator; MHC class I
interferon-gamma; interleukin-4; vaccine; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class II trans activator (CIITA) 151 deletion mutant. Class II trans activator; MHC; CIITA; autoLimune disease; treitansplantation; xenograft; major histocompatibility complex; gene therapy; arthritis; ribozyme; 151 deletion mutant.
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16-APR-1998.
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WPI; 98-559115/48.
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22-APR-1997; FR-0(
(TRGE ) TRANSGENE
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; FR-004954.
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larity 55.6%;
Conservative
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/note= "wild .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ′label=
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Pred.
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1. No. 2.29e+02;
Mismatches 0;
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                      activator
CIITA is
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21-APR-1998; 22-APR-1997; (TRGE) TRANS

400968. FR-004954.

TRANSGENE SA

8

EP-874049-A1.

28-OCT-1998

HOMO

sapiens.

interferon-gamma;

CIITA (class II transactivator) type II protein CIITA gene; class II transactivator; MHC class I

interleukin-4;

vaccine;

II molecule;
er treatment.

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                                                                                                                                                                                                                                                                                            Query Match
Best Local s
Matches
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Best I
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Matches
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2 SGTMRTRHSTG
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                                                                                                                                                         W80312 standard;
W80312;
                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1; 16pp; Japanese.
Transforming a bacteria with the PPC encoding sequence intensifies CO2 fixation ability. Other PPC genes may also be found by hybridisation with an A.nidulans derived probe.
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N-PSDB; N60838.
                                                                                                                                              01-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                            PPC gene of cloned photosynthetic microorganisms intensifying photosynthesis carbon di:oxide-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KOHZ/) KOHZUKI H. WPI; 86-115948/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.nidulans phosphenol pyruvic acid carboxylase gene PPC; photosynthesis; pA181; pA171; pA172; pA172A.
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                                                                                                                                                                                                                                                                                            h 48.5%;
Similarity 54.5%;
6; Conservative
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Similarity 55.6%;
S; Conservative
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                                                                                                                                                                       Protein; 1106
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Pred.
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No. 2.29e+02;
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. No. 2.29e+02;
Mismatches 3;
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This represents a class II trans activator (CIITA) polypeptide. When the N-terminal region of the CIITA is deleted, it can be used for reducing the expression of major histocompatibility complex (MKC) class II antigens. A ribozyme targeted to-bases 1159-1161 (GUA) of human CIITA mRNA, or corresponding target in other species and the CIITA polypeptide can be used to reduce expression of MHC class II antigens, particularly croman to autoimmune disease (e.g. arthritis and diabetes) or to the croman animals intended as source of xenografts. The ribozyme can the CIITA polypeptide may be generated in vivo by gene therapy, using the encoding nucleic acids targeted for localised suppression of the climanne response. Material from transgenic animals in which at least some cells are stably transfected with the CIITA encoding nucleic acids are used for animal-to-human transplantation. The CIITA polypeptide coused for animal-to-human transplantation. The clira the express them constitutively or after lymphokine induction. It has no transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g. as primers for enzymatic amplification, as detection probes or as inhibitors of expression of genes encoding MHC in dendritic cells claim 10; Pages 58-61; 86pp; French.

The present sequence represents type II CIITA (class II transactivator) protein. The products can be used to treat diseases for which enhanced expression of genes coding for MHC class II molecules is desired, especially where the enhanced expression is desired in dendritic cells or after induction by a cytokine, especially interferon gamma or interleukin-4. Inhibitors of the gene or protein can be used to treat diseases for which reduced expression of genes coding for MHC class II molecules is desired or can be used as vaccines, especially for cancer treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class II trans activator (CIITA) polypeptide.

Class II trans activator; MHC; CIITA; autoimmune disease; treatment; transplantation; xenograft; major histocompatibility complex; diabetes; gene therapy; arthritis; ribozyme.
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DNA encoding MHC class II trans-activator polypeptide(s) -e.g. as primers for enzymatic amplification, as detection e.g. as primers for enzymatic amplification, as detection
                                                                                                                                                                                                                                                                                                                               antigen expression - and ribozyme directed to trans-activator mRNA, related nucleic acid, vectors, transformed cells and antibodies, used for treating auto-immune disease and to inhibit xeno-graft
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16-APR-1998.
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W57056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-OCT-1997; G02751.
21-MAR-1997; GB-005911.
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llarity 55.6%;
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2.29e+02;
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class II
Sequence
                                                                                                                                                                                                                                                                                                                                      Class II transactivator protein.

Class II transactivator protein; MHC class II;

Class II transactivator protein; MHC class II;

Insulin dependent diabetes; multiple sclerosis; lupus erythematosis;

Insulin dependent diabetes; multiple sclerosis; lupus erythematosis; lupus erythematosis; lupus erythematosis; lupus erythematosis; lupus erythematosis; lupus erythem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding MHC class II trans-activator polypeptide(s) - useful e.g. as primers for enzymatic amplification, as detection probes or as inhibitors of expression of genes encoding MHC in dendritic cells Claim 31; Pages 62-66; 86pp; French.

The present sequence represents type III CIITA (class II transactivator) protein. The products can be used to treat diseases for which enhanced expression of genes coding for MHC class II molecules is desired, especially where the enhanced expression is desired in dendritic cells or after induction by a cytokine, especially interferon-gamma or interleukin-4. Inhibitors of the gene or protein can be used to treat diseases for which reduced expression of genes coding for MHC class II molecules is desired or can be used as vaccines, especially for cancer treatment.
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08-DEC-1995 (first entry)
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R72452 standard; Protein; 1130
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22-APR-1997;
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1130 AA;
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Llaritý 55.6%;
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261..322
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If gene encoding a protein displaying class II trans-activator protein encoding a protein displaying class II trans-activator protein the protein sequence is encoded by the gene represented in Q88110. CC This protein sequence is encoded by the gene represented in Q88110. CC This protein is a class II transactivator (CIITA) essential for the CC control of MHC class II gene expression in Blymphocytes. The DNA CC sequence has two in frame start codons. The first of these is at position CC in and acts as the translation initiation site. The second is present CC (at position 188) in the context of a perfect Kozak box and may also CC contains three stretches rich in proline/serine/threonine. It also CC contains three stretches rich in proline/serine/threonine. It also CC contains a region rich in glutamate/aspartate (an accidic region) and an ATP/GTP binding cassette. The acidic regions followed by three stretches CC arctivation domain. There is also a leucine-rich region around amino CC acids 979 to 1061 that shows weak homology with the N terminal portion of a yeast RNA binding protein. The protein can be used for the CC sequence can be used to treat diseases where a decrease in the level of cartivation. The cells II genes is desired e.g. insulin dependant CC artheirs, multiple sclerosis, lupus erythematosis and rheumatoid
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Best Local s
Matches
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19-APR-1995.
26-AUG-1994; 113378.
26-AUG-1993; EP-113665.
(MACH/) MACH B F.
Mach BF;
auto:immune disorders
Example 1; Page 36-41; 64pp; English.
Example 1; Page 36-41; 64pp; English.
A genomic DNA sequence (T18028) codes for the class II
transactivator, CIITA (R81569), a protein essential for activation
of transcription of MHC class II genes. The CIITA transcription
activation domain provides useful information for identifying cpds
which inhibit CIITA-dependent transcription. Such cpds. are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; Q88110.
                                                                                                                                                                                                                                                                                                                                                                                                   Class II transactivator.
CIITA; class II transactivator; transcription;
major histocompatibility complex class II; aut
                                                                                                                                                                                                                                                    WO9606107-A1.
29-FEB-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                Methods which inhibit transcription activation by CIITA - causes inhibition of MHC class II gene expression, used in therapy of
                                                                                                                                                   N-PSDB; T18028
                                                                                                                                                                   24-AUG-1994; US-295502.
(HARD ) HARVARD COLLEGE.
Douhan J, Glimcher LH,
WPI; 96-151325/15.
                                                                                                                                                                                                                     22-AUG-1995;
24-AUG-1994;
                                                                                                                                                                                                                                                                                                         domain
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                                                                                                                                                                                                                                                                                                                                                           Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R81569 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      797 qpgtirarq
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Similarity 55.6%;
5; Conservative
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301..1130
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                                                                                                                                                                                                                                                                                                                                           352
                                                                                                                                                                                                                                                                                         "interaction domain"
                                                                                                                                                                                                                                                                                                                        "transcription activation
                                                                                                                                                                                      Zhou
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Pred. No.
4; Misma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .29e+02;
                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a type I CITA (class II transactivator) protein. The products can be used to treat diseases for which enhanced expression of genes coding for MHC class II molecules is desired, especially where the enhanced expression is desired in dendritic cells or after induction by a cytokine, especially interferon-gamma or interleukin-4. Inhibitors of the gene or protein can be used to treat diseases for which reduced expression of genes coding for MHC class II molecules is desired or can be used as vaccines, especially for cancer treatment.
                                                           11-FEB-1993;
06-JUN-1995;
(GEMV ) GENEN
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Sequence 1130 AA;
          Barnett
Solheim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding MHC class II trans-activator polypeptide(s) - useful e.g. as primers for enzymatic amplification, as detection probes as inhibitors of expression of genes encoding MHC in dendritic ce Claim 10; Pages 53-57; 86pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
EP-874049-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CIITA (class II transactivator) type I protein.
CIITA gene; class II transactivator; MHC class II molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 14
W80311 standard; Protein; 1207
                                                                                                                                                                                                                                                        Alpha-amylase protein variant M197T. PCR primer; alpha-amylase; variant; oxidative stability.
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22-APR-1997;
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                                                                                                                                                                                                               US5849549-A.
                                                                                                                                                                                                                                      Bacillus licheniformis.
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W73510;
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                                                                                                                                      10-FEB-1994;
                                                                                                                                                             06-JUN-1995;
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LEB-1994; US-194664.
-FEB-1993; US-016395.
JUN-1995; US-468698.
V) GENENCORTINT.
'tt CC, Mitchire'
'm LP;
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QSGTMRTRH 9
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larity 55.6%;
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FR-004954.
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Pred. No. 2.29e+02;
4; Mismatches 0;
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Pred.
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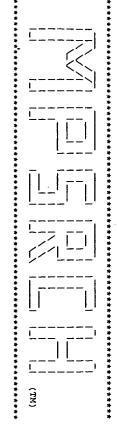
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Starch liquefaction - using mutant Bacillus alpha-amylase
Disclosure; Fig 4a; 56pp; English.
This sequence represents the M197T variant of the Bacillus
This sequence represents the M197T variant of the Bacillus
(I then invention, for liquefying a granular starch slurry from
the method of the invention, for liquefying a granular starch slurry from
a wet or dry milling process at a PH of 4 to less than 6, that comprises
adding a mutant Bacillus alpha-amylase to the slurry, optionally adding
an antioxidant, and reacting the slurry until the starch is liquefied.
The alpha-amylase has a substitution of Thr. Leu, Asn or Asp for a Met
residue corresponding to M15 in B. 1tcheniformis alpha-amylase.
Alternatively the alpha-amylase has a substitution of Leu or Ala for a
residue corresponding to M197 in B. 1icheniformis alpha amylase. Mutants
such as M197L and M15L have enhanced oxidative stability at PH 5.
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Gaps ö Score 47; DB 38; Length 483; Pred. No. 2.87e+02; 3; Mismatches 3; Indels Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative

69 qkgtvrtkygtkg 81 | ||:||: :| | | QSGTMRTRHSTGG 13 g

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Search completed: Fri Jun 11 17:54:36 1999 Job time : 106 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Fri Jun 11 17:57:22 1999; MasPar time 4.34 Seconds 138.367 Million cell updates/sec

Description:
Perfect Score:
Sequence: Title: >US-08-991-628-7 (1-15) from US08991628.pep 99 1 QSGTMRTRHSTGGTN 15

Scoring table: PAM 150 Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Database:

Statistics: Mean 23.847; Variance 29.890; scale 0.798

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

222 232 232 232 232 232 232 232 232 232	Result
44446000000000000000000000000000000000	Score
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999 453 1597 4797 534 537 537 537 537 537 537 537 537 140 481 481 495 2318 495 572 572 572 572 572 573 573 673 673 673 673	Length
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desmoglein 3 precurso keratin 10, type I, c sol protein, large sp DNA-directed RNA poly protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina ps9(xfyn) - xiphophor protein-tyrosine kina gene m3 protein - Lac p-Aminobenzoic acid s glycinin G3 recursor glycinin G3 precursor glycinin G1 precursor glycinin G1 precursor glycinin G1 precursor minoglycoside-N-acet hemagglutinin-neuraminoth 3 protein - mouse H-2K-s-mouse H-2K-sml - mouse hypothetical protein	Description
1.83e-01 3.92e-01 6.39e-01 1.04e+00 1.04e+00 1.04e+00 1.04e+00 2.69e+00 6.80e+00 6.80e+00 6.80e+00 6.80e+00 1.07e+01 1.07e+01 1.07e+01 1.68e+01 1.68e+01 1.68e+01 1.68e+01 1.68e+01 1.68e+01 1.68e+01 1.68e+01 1.68e+01	

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47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5
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tensin - chicken (fra	probable membrane pro	toxR-regulated lipopr	alpha-amylase (EC 3.2	nucleocapsid protein	bam protein - fruit f	filaggrin precursor -	probable ribosomal pr	extracellular nucleas	invasion-inducing pro	coatomer complex alph	MHC class II transact	phosphoenolpyruvate c	cell division control	phosphoprotein - fiss	nitrate reductase (EC	protein-serine/threon	hypothetical protein	exo-alpha-sialidase (bindin fertilization	transcription factor	scytalone dehydratase
4.03e+01	4.03e+01	4.03e+01	4.03e+01	4.03e+01	4.03e+01	4.03e+01	4.03e+01	2.61e+01 2.61e+01	2.61e+01	2.61e+01	2.61e+01										

Query Match Best Local Simil Matches 15;	910-938 937-966 110,180,545 SUMMARY #	50-615 52-157 160-267 270-383 390-495 496-598 616-639 640-999	FEATURE 1-23 24-49 50-999	#gene #cross-refe #map_position 1 CLASSIFICATION # KEYWORDS	#cross-references MUID: #accession A41088 #accession Lype mRNA ##residues 1-99 ##cross-references G	ACCESSIONS A REFERENCE A #authors A #journal C #title A	RESULT 1 ENTRY TITLE TITLE dALTERNATE_NAMES PORGANISM #
100.0%; Score 99; DB 1; Length 999; Similarity 100.0%; Pred. No. 1.83e-11; 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	desmoglein repeat #label DG1\ desmoglein repeat #label DG2\ desmoglein repeat #label DG2\ g_site carbohydrate (Asn) (covalent) #st cted #molecular-weight 107502 #checksum 831	#domain extracellular #status predicted #label EXT\ #domain cadherin repeat homology #label CR1\ #domain cadherin repeat homology #label CR2\ #domain cadherin repeat homology #label CR3\ #domain cadherin repeat homology #label CR4\ #domain cadherin repeat homology #label CR5\ #domain transmembrane #status predicted #label TMY\ #domain intracellular #status predicted #label INT\	#domain signal sequence #status predicted #label SIG\ #domain propeptide #status predicted #label PRO\ #product desmoglein homolog #status predicted #label	CS GDB:DSG3 ##cross-references GDB:134030; OMIM:169615 p_position 18q12.1-18q12.2 FICATION #superfamily cadherin; cadherin repeat homology calcium binding; cell adhesion; duplication; glycoprotein; CRITICATION calcium binding; cell adhesion; duplication; glycoprotein;	us vulgaris, a disease of cell adhesion. 92069753 9 ##label AMA B:M76482; NID:g190751; PID:g190752	18-Sep-1998 A41088 A41088 A41088 A6108 A6108 A6108 A6108 A67-869-877 A610 A67-869-877 A610 A67-869-877 A610 A67-869-877 A610 A67-869-877 A67-861 A67-869-877	IJHUG3 #type complete desmoglein 3 precursor - human pemphigus vulgaris antigen #formal_name Homo sapiens #common_name man 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change

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                                                                                #accession
                                                                                            structural brain gene *cross-references MUID:91334436
                                                                                                                                                           #journal
                                                                                                                                                                                                 #authors
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IFICATION #superfamily cytoskeletal keratin
tos coiled coil; heptad repeat; interr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type mRNA
##residues 1-453 ##label DAR1
##coss-references EMBL:M19156
# the sequence from Fig. 3 is inconsistent with the
nucleotide sequence from Fig. 2 in having additional
residues ile-Lys-Ile-Arg-Leu after 313-Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     408 GGGLRGRHSGGGSS 421
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##residues 1-1597 ##label DEL
##cross-references GB:M64084; NID:g2760822; PID:g158483
The sol (small optic lobes) mutation eliminates certain classes
                                                        ##molecule_type mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 57.6%; Similarity 50.0%; 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Darmon, M.Y.; Semat, A.; Darmon, M.C.; Vasseur, M. submitted to the EMBL Data Library, May 1988 $14669
                                                                                                              Proc. Natl. Acad. Sci. U.S.A. (1991) 88:7214-7218
Molecular cloning and analysis of small optic lobes
structural brain gene of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Darmon, M.Y.; Semat, A.; Darmon, M.C.; Vasseur, M. Mol. Biol. Rep. (1987) 12:277-283
Sequence of a cDNA encoding human keratin No 10 selected according to structural homologies of keratins and their tissue-specific expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytokeratin 10
#formal_name Homo sapiens #common_name man
30-Sep-1991 #sequence_revision 31-Dec-1991
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#length 453 #checksum 131
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$14666
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keratin 10, type I,
                                                                                                                                                                                                                                                                      #formal_name Drosophila melanogaster
30.Jun-1992 #sequence_revision 30-Jun-1992 #text_change
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                                                                                                                                                                                           Delaney, S.J.; Hayward, D.C.; Barleben, F.; Fischbach, K.F.;
                                                                                                                                                                                                                   A41146
                                                                                                                                                                             Miklos,
                                                                                                                                                                                                                                                                                                                melanogaster)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #domain head (fragment) #status predicted #label HEA\
#domain helical rod #status predicted #label ROD\
#domain tail #status predicted #label TAI
                                                                                                                                                                           G.L.G
                                                                                                                                                                                                                                                                                                                                                  #type complete
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                                                                                                                                                                                                                                                                                                                                large splice form -
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Pred. No. 3.92e-01;
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                                                                                                                                                                                                                                                                                                                                fruit fly (Drosophila
                                                                                                                                   small optic lobes, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 453;
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FEATURE
12-29
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SUMMARY
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CLASSIFICATION
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Best Local Similarity
Matches 8; Conser
Query Match
Best Local Similarity
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649-667
673-702
713-730
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                                                                                                                                                                        #genetic_code
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|p_position 19F4
                                                                                                                                                                                                                              ##molecule_type DNA
##residues 1-124 ##label KA2
##cross-references EMBL:X66452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##cross-references EMBL:X66452; NID:g9314; PID:g578408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues
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                                                                                                                                                                          RPB1
SGC9
                                                        DNA binding; nucleotidyltransferase;
transcription; zinc finger
#length 478 #checksum 3090
                                                                                                               *superfamily human DNA-directed RNA chain
                                                                                                                                                                                                                                                                                                                                                  Kaufmann, J.; Florian, V.; Klein, A.
Nucleic Acids Res. (1992) 20:5985-5989
Nucleic Acids Res. (1992) 20:5985-5989
TGA cysteine codons and intron sequences in conserved nonconserved positions are found in macronuclear RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S33886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene dosage as a possible major determinant for equal expression levels of genes encoding RNA polymerase
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DNA-directed RNA polymerase (EC
RPB1 - Euplotes octocarinatus
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alternative splicing; brain; zinc finger
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08-Dec-1993 #sequence_revision 10-Nov-1995 #text_change
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Nucleic Acids Res. (1992) 20:4445-4450
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#region zinc finger CCCC motif\
#domain calpain catalytic domain homology #label CALP\
#domain calpain catalytic domain benedicted
#active_site Cys, His, Asn #status predicted
#active_site Cys, His, Asn #status predicted
#active_site Cys, His, Asn #status predicted
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#region zinc finger CCCC motify
#region zinc finger CCCC motify
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  56.6%;
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Score
Pred.
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Pred. No. 3.92e-01;
3; Mismatches 2
  N 56
  : DB 2; I
. 6.39e-01;
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                  Length 478
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FEATURE
89-138
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Best Local S
Matches
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266-524
274-282
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##cross-references GB:M27266; NID:g193357; PID:g309241
##cross-references GB:M2726; NID:g193357; PID:g309241
##cross-references GB:M2726; NID:g193357; PID:g309241
##cross-references GB:M2726; NID:g193357; PID:g309241
##cross-references GB:M2726; NID:g193357; PID:g309241
##cross-references GB:M27266; NID:g193357; PID:g19309241
##cross-references GB:M27266; NID:g193357; PID:g19309241
##cross-references GB:M27266; NID:g193357; PID:g19309241
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##cross-references GB:M27266; NID:g19309241
##cross-ref
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                                                                                                                                                    ##molecule_type mRNA
#*residues 1-534 #*label
##cross-references EMBL:X52841
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      #cross-references
                                           ##molecule_type mRNA
                         #residues
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Similarity 57.1%;
8; Conservative
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                                                                                                                                                                                                                                    J.; Yamamoto, T., ..., NewHoon, L.; Sarkar, Oncogene (1993) 8:823-831
A novel Yes-related kinase, Yrk, is expressed levels in neural and hematopoietic tissues. nces MUID:93205395
                                                                                                                                                                                                                                                                                                                                                                                                                sy3568 #type complete
protein-tyrosine kinase (EC 2.7.1.112) fyn - ch:
#formal_name Gallus gallus #common_name chicken
31-Dec-1993 #sequence_revision 02-Aug-1994 #text
08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A44991 #type complete
protein-tyrosine kinase (EC 2.7.1.112) fyn -
kinase-related transforming protein (fyn)
fformal_name Mus musculus #common_name house
03.Jun-1993 #sequence_revision 30-Sep-1993 #t
08-Sep-1997
                                                                         submitted to S36351
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New Biol. (1989) 1:66-74
Expression of a novel form of the
hematopoietic cells.
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                                                                                                                Sudol, M.
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$33568
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es EMBL:X52841; NID:g62861;
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#domain SH2 homology #label SH2\
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                                                                                           the
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Pred. No. 1.04e+00;
4; Mismatches 2
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      PID: g62862
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Best Local Similarity 57.1%;
Matches 8; Conservative
#authors #journal
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Similarity 57.1%;
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  Hannig, G.; Ottilie, S.; Schartl, Oncogene (1991) 6:361-369
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#journal Oncogene (1990) 5:369-376
#title Structure and expression of fyn
#cross-references MUID:90191723
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151592 *type complete
p59(XTp) - Xiphophorus helleri
#formal_name Xiphophorus helleri
04-Sep-1997 *sequence_revision 0
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homology; St2 homology; St3 homology
ATP; phosphoprotein; phosphotransferase; F
transforming protein; tyrosine-specific
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protein-tyrosine kinase (EC 2.7.1.112) fyn -
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#domain SH2 homology #label SH2\
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#region protein kinase ATP-binding moti
gth 537 #molecular-weight 60846 #chec)
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#region protein kinase ATP-binding motif\
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#binding_site phosphate (Tyr) (covalent) #status
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Pred. No. 1.04e+00;
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Pred. No. 1.04e+00;
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ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;.
                                                                                                       STRAIN-CV. COLUMBIA;

BARMON G., LANGSTON Y., STONEKING T., DRONE K., AMES

BARMON G., LANGSTON Y., STONEKING T., DRONE K., AMES

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"A retrotransposon family from
GENE 215:241:249(1998).
EMBL; AF03C881; G3510505; -.
                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                        SEQUENCE FROM N.A. STRAIN-CV. COLUMBIA;
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"The Arabidoybis thaliana Genome Sequencing Project.";
SNBMITTED (JÜL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
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Pred. No. 1.35e+00
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01-AUG-1998
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O53240;
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SEQUENCE FROM N.A.
SERAIN-CV. COLUMBIA;
WATERSTON R.;
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF077408; G3319363; -.
SEQUENCE 973 AA; 112369 MW; F6086EE2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-H37RV;
OLIVER K., HARRIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYCOBACTERIUM TUBERCULOSIS.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIADE;
ACTINOMYCETALES; CORYNEBACTERINEAB; MYCOBACTERIACEAE; MYCOBACTERIACEAEE; MYCOBACTERIACEAEEE
                                                                                                            330AA LONG
PH1720.
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BARRELL B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OLIVER K., HARRIS D.;
SUBMITTED (JAN-1998)
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01-JUN-1998 (TREMBLREL: 06, I
01-NOV-1998 (TREMBLREL: 08, I
HYPOTHETICAL 18.2 KD PROTEIN
                                                                       PYROCOCCUS
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PHILIPP W.J., POUL
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Similarity 87.5%;
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07, LAST SEQUENCE UPDATE)
09, LAST NANOTATION UPDATE)
N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE
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B., BERGH
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1; Misma
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Q50378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAWARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y., YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y., SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y., FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of mycobacteria: the f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete Sequence and Gene Organization of the Genome of Hyper-thermophilic Archaebacterium, Pyrococcus horikoshii DNA RES. 5:55-76(1998).
EMBL: AP000007; D1031777; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-OT3;
MEDLINE; 98344137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYCOBACTERIUM SMEGMATIS.
BACTERIA; FIRMICUTES; ACTINOBACTERIA;
ACTINOMYCETALES; CORYNEBACTERINEAB; M
                                                                                                                                                                                                   01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 62.8 KD PROTEIN.
                                                                                                                                                                                                                                                                                                066695;
                                                                                                                                                                                                                                                                                                                     066695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOL. MICROBIOL, 14:557-569(1994).
EMBL; U10425; G595404; -.
PFAM; PF00551; formyl_transf; 1.
SEQUENCE 360 AA; 41130 MW; A81D7F3B.CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-MC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FERRIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIKUCHI
MEDLINE; 98196666.
DECKERT G., WARREN P.V.,
GRAHAM D.E., OVERBEEK R.
                                                                      STRAIN-VF5
                                                                                       SEQUENCE FROM N.A
                                                                                                                                      BACTERIA;
                                                                                                                                                       AQUIFEX AEOLICUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oathways.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDLINE; 95191405.
                                                                                                                                                                                                                                                                                                                                                                                                            241 RALSDPYPNAYTY
|:|:: | ·:||:
3 RTLNNRYTGPYTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 54.1%;
Local Similarity 38.5%;
hes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 RGLNLRFTSDYNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXOCHELIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 7; Conser
                                                                                                                                    AQUIFICALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    330 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.1%;
larity 53.8%;
Conservative
                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D1031777;
AA; 37168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          f genes
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                                                                                                                                    AQUIFICACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          involved i exochelin
GAASTERLAND T., YOUNG W.G., LENOX A.L., SNEAD M.A., KELLER M., AUJAY M., HUBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 59; DB 1; I
Pred. No. 3.20e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 59; I
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D80618ED CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; ACTINOBACTERIDAE; MYCOBACTERIACEAE; M
                                                                                                                                    AQUIFEX
                                                                                                                                                                                                                                                                                                                     531
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UKU Y.,
OGUCHI A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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JLT 10 029749 029749; 029749; 01-JAN-1998

PRELIMINARY;

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RESULT

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SOLUTION OF THE PROPERTY OF TH
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Best Local s
Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE; 92260626.
MARTINEZ M.A. DOPAZO J., I
DOMINGO E., KNOWLES N.J.;
Tevolution of the capsid pi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete aeolicus.";
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01-NOV-1996
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Q01124;
                                                                                                                                                                                                                            EMBL; MS
PFAM; PF
COAT PRO
NON_TER
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., FELDWAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; AE000686; G2983043; -.

HYPOTHETICAL PROTEIN.

SEQUENCE 531 AA; 62830 MW; 585EBE7E CRC32;
                                                                                                                                                               DOMAIN
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                           Substitutions over six decades.;

J. VIROL. 66:3557-3565(1992).

-!- THE COAT PROTEIN VPI CONTAINS THE MAIN ANTIGENIC DETERMINANTS
THE VIRION; THEREFORE, CHANGES IN ITS SEQUENCE MUST BE
RESPONSIBLE FOR THE HIGH ANTIGENIC VARIABILITY OF THE VIRUS.
-!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VPI, VP3, AND VP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOOT-AND-MOUTH DISEASE VIRUS (APHTHOVIRUS C).
VIRUSES; SSRNA POSITIVE-STRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-VF5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COAT PROTEIN VP1
                                           125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APHTHOVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 TLKNRLENPYTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 TLNNRYTGPYTF
                                                                                                                                                                                                                                                                                  VP3, AND VP4.
; M90377; G210394;
d; PF00073; rhv; 1.
                                         RVLATRYTGTTTY
                                                                                                                                                                                                                                                                       PROTEIN.
  RTLNNRYTGPYTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigenic variation without
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                                                                                                     Similarity
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5 (TREMBLREL. 01, 1
} (TREMBLREL. 08, I
N VP1 (FRAGMENT).
                                                                                                                                                               188
211
211
                                                                               53.2%;
larity 53.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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211
211
211
23028 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HERNANDEZ
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Pred.
1; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                               Score 58; DB 14; L
Pred. No. 4.88e+00;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (STRAIN C5
                                                                                                                                                                                                          ANTIGENIC A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIRUSES,
                                                                                                                                                                 B1B474E6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59; DB 2; I
No. 3.20e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     accumulation
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78)
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                                                                                                                                                                                                          SIMILARITY).
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acid
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SUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 87.2 KD PROTEIN
HYPOTHETICAL 87.2 KD PROTEIN
BARLEX STRIPE MOSAIC VIRUS (BSMV)
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; HORDEIVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 90066400.

KOZLOV YU.V., AFANAS'EV B.N., RUPASOV V.V.; GOLOVA YU.B.,

KULABVA O.I., DOLVAV V.V., ATABEKOV I.G., BAEV A.A.;

"Primary structure of RNA 3 of barley stripe mosaic virus and its variability.";
                                                                                                                                                                      AZZARIA M., GOSZCZYNSKI B., CHUNG M.A., KALB J.M., MCGHEE J.D.;
SUBMITTED (APR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 58; DB 14; Length 770; Pred. No. 4.88e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 53.2%; Score 58; DB 5; Length 506; Local Similarity 50.0%; Pred. No. 4.88e+00;
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MORTIMORE B.;
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U51163; G1256430; -.
EMBL; 292833; E1346571; -.
PFAM; PF00250; FOIK_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         076025 PRELIMINARY; PRT; 80 AA. 076025; 01-NOY-1996 (TREMBLREL. 01, CREATED) 01-NOY-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) 01-NOY-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) ENVELOPE GLYCOPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN IMMUNODEFIÇIENCY VIRUS TYPE 1 (HIV-1).
VIRUSES; RETROID VIRUSES; RETROVIRIDAE; LENTIVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.88e+00;
atches 2;
                                                                                                                                                                                                                                                                                                                                        PFAM; PF00250; FOTK head; 1.

PROSITE; PS00657; FORK_HEAD_1; 1.

PROSITE; PS00658; FORK_HEAD_2; 1.

SEQUENCE 506 AA; 55426 MW; 54119AA3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  770 AA; 87176 MW; 34477E66 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
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EMBL. X52774, 6297555;
PFAM: PRO0978; RNA_dep_RNApol2; 1.
HYPOTHETICAL PROTEIN.
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ses 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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                                        CAENORHABDITIS ELEGANS
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3 RTLNNRYTGPYT 14
                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                               STRAIN-N2;
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Q07117 .
Q07117; ~
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                                                                                                                                                             SEQUENCE FROM N.A.

STAANN-VC-16 / DSM 4304 / ATCC 49558;

KEDINE; 98049343.

A KEDEN H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,

A KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,

A RICHARDSON D.L., KERTAYAGE A.R., GRAHAM D.E., KYRPIDES N.C.,

A RICHARDSON D.L., KERTAYAGE A.R., GRAHAM D.E., KYRPIDES N.C.,

A RICHARDSON D.L., KERTAYAGE A.R., GWILL S.,

A KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,

A PETERSON S., REICH C.I., MONEIL L.K., BADGER J.H., GLODEK A., ZHOU I.,

OVERBEEK R., GOCAYLE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,

A OVERBEEK R., GOCAYLE B.MANIACH P., KAINE B.P., SYKES S.M.,

A RADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,

NEMBER R., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
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BACTERIA; CYANOBACTERIA; NOSTOCALES; NOSTOCACEAE; ANABAENA
                                                                                                  ARCHAEA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE;
ARCHAEOGLOBUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 58; DB 1; Length 332;
Pred. No. 4.88e+00;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 58; DB 2; Length 444;
Pred. No. 4.88e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus."; NATURE 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCC 7120;
J., SCAPPINO L.A., HASELKORN R.;
J.A.1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
55; G1185622; -
J.48; oxidored_nitro; 1.
444 AA; 48332 MW; 9C962756 CRC32;
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LAST SEQUENCE UFDATE)
LAST ANNOTATION UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
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                 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION
NITRATE REDUCTASE, GAMMA SUBUNIT, PUTATIVE
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017381 PRELIMINARY;
017381, 01788, 01788, 01.01, 01.00-1996 (TREMBLREL. 01, LI
01-NOV-1996 (TREMBLREL. 01, LI
01-AUG-1998 (TREMBLREL. 07, LI
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cal Similarity 46.2%;
6; Conservative
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Best Local Similarity 50.0%;
Matches 6; Conservative
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24145 PRELIMINARY;
044145;
01-NOV-1996 (TREMBLREL. 0
01-NOV-1996 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
NIFN.
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#journal
#title
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89-138
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#title Conservation of structure and expression of the c-yes and fyn
genes in lower vertebrates.
#cross-references MUID:91187435
#accession 151592.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type mRNA
##residues 1-183,'S',185-436,'R',438-537 ##label KAWI
##cross-references GB:M14676; NID:g338227; PID:g338228
##cote the authors translated the codon GAA for residue 265 as
##note Gln and GGA for residue 278 as Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kawakami, T.; Pennington, C.Y.; Robbins, K.C.
Mol. Cell. Biol. (1986) 6:4195-4201
Isolation and oncogenic potential of a novel human src-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVHUSY #type complete protein-tyrosine kinase (EC 2.7.1.112) fyn, splice form B
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                                                                                                                                                                                                                                                                                                                                                                                                                #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##cross-references GB:M20284; NID:q182842; PID:q182843
##experimental_source clone pFYN(c)-11; termination mutant p56(fyn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #authors Semba, K.; Nishizawa, M.; Miyajima, N.; Yoshida, M.C.; Sukagawa, J.; Yamanashi, Y.; Sasaki, M.; Yamamoto, T.; Tukegawa, K. Tooshina, K. Tooshina, K. Proc. Natl. Acad. Sci. U.S.A. (1986) 83:5459-5463 #title yes-related protooncogene, syn, belongs to the protein tyrosine kinase family.
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#domain protein kinase homology #label KIN
#length 537 #molecular-weight 60447 #checksum 621
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                                                                                                              ##molecule_type mRNA
##residues
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*cross-references GB:M14333; NID:g181171; PID:g181172
                                                                                                                                                                                                                                                                                             ##cross-references EMBL:X54971; NID:g64481; PID:g64482
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#accession A25389
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larity 57.1%;
Conservative
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#authors
#journal
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149-246
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*superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology alternative splicing; APP; autophosphorylation; blocked amino end; lipoprotein; momesr; myristylation; phosphoprotein; phosphotransferase; proto-oncogene; thiolester bond; transforming protein; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Noble, M.E.M.; Musacchio, A.; Saraste, M.; Courtneidge, S.A.;
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#domain SH2 homology #label SH2\
...#domain protein kinase homology #label KIN\
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#submission submitted to the Brookhaven Protein Data Bank, May 1995
#cross-references PDB:1FYN
#contents annotation; X-ray crystallography, 2.3 angstroms, residues
81-142
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Mature Struct. Biol. (1994) 1:546-551
High-resolution crystal structures of tyrosine kinase SH3
domains complexed with proline-rich peptides.
                                             *authors Noble, M.; Musacchio, A.; Saraste, M.; Wierenga, R. *submission submitted to the Brookhaven Protein Data Bank, May 1993 #cross-references PDB:1SHF #contents
                                                                                                                                                                                                         Peters, D.J.; McGrew, B.R.; Perron, D.C.; Liptak, L.M.;
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#journal EMBO J. (1993) 12:2617-2624
#title Crystal structure of the SH3 domain in human Pyn; com
of the three-dimensional structures of SH3 domains
tyrosine kinases and spectrin.
#cross-references MUID:93327750
                                                                                                                                                                                                                              #Journal Dacogene (1990) 5:1313-1319
#title In Vivo phosphorylation and membrane association of proto-oncogene product in IM-9 human lymphoblasts.
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                                                                                                                                                  #authors Arhin, F.F.; Vining, L.C.
#journal Gene (1993) 126:129-133
#title Organization of the genes encoding p-aminobenzoic
#synthetase from Streptomyces lividans 1326.
#cross-references_MUID:93231526
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##cross-references GB:M64859; NID:g153393; PID:g153394
This enzyme participates in p-aminobenzoic acid biosynthesis.
                                                                                                            ##molecule_type DNA
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gene m3 protein - Lactococcus phage bIL170
#formal_name Lactococcus phage bIL170
24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change
24-Mar-1999
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ilarity 60.0%;
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#superfamily anthranilate synthase component I carbon-carbon lyase; oxo-acid-lyase; p-aminobenzoate
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14-Jul-1994 #sequence_revision 14.
21-Aug-1998
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p-Aminobenzoic acid synthetase (EC 4.1.3.-)
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#journal Nucleic Acids Res. (1989) 17:4388
#title The glydinin Gy(3) gene from soybo
#cross-references MUID:89296500
                                                                                                                                                                                                                     #authors Nielsen, N.C.; Dickinson, C.
Scallon, B.J.; Fischer, R.
Goldberg, R.B.
#journal Plant Cell (1989) 1:313-328
#title Characterization of the glyo
#cross-references MUID:92393391
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##residues 1-484 ##label
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Similarity 58.3%;
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51.5%;
Similarity 58.3%;
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glycinin G3 precursor - soybean
#formal_name Glycine max #common_name soybean
21-Nov-1993 #sequence_revision 19-Jan-1996 #te
03-May-1996
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#superfamily glycinin
#length 481 #molecular-weight 54241
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#formal_name Glycine max #common_name soybean
28-Feb-1990 #sequence_revision 28-Feb-1990 #te
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                                                                                                        ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                      Query Match 51.5%;
Best Local Similarity 58.3%;
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107-317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *duthors Kitamura, Y.; Arahira, M.; Itoh, Y.; Fukazawa, C.

*journal Nucleic Acids Res. (1990) 18:4245

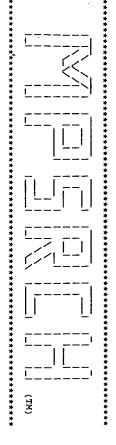
*title The complete nucleotide sequence of soybean glycinin A2B1a

*title gene spanning to another glycinin gene AlaBlb.

*cross-references MUID:90332420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #journal
#title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors
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                                                                                                                                                                                                                                                                          318 TMRLRHNIGQTS 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues 481-495 ##label KIT
##cross-references EMBL:X53404; NID:g18522; PID:g18523
The source of this protein was cotyledon tissue taken 38 days after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues 1-495 ##label NEG
##cross-references GB:X02985; NID:918614; PID:918615
##exper1mental_source cv. Bonminori
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             $10851 #type complete
glycinin Gl precursor - soybean
glycinin AlaBx
glycinin chain Ala; glycinin chain Bx
#formal_name Glycine max #common_name soybean
21.Nov-1993 #sequence_revision 19-Jan-1996 #text_change
08-Sep-1997
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Nucleic Acids Res. (1985) 13:6719-6731
A CDNA clone encoding a glycinin A-la subunit precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycinin chain Alabx precursor - soybean
11S globulin; glycinin Alabx
#formal_name Glycine max #common_name soybean
31-Max-1988 #sequence_revision 31-Max-1988 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seed; storage protein
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                                                                                                                                                                                                                                                                                                                                                                                                #product glycinin chain Bx #status predicted #label GLB\
#disulfide_bonds #status predicted
#th 495 #molecular-weight 55506 #checksum 8518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #domain signal sequence #status predicted #label SIG\
#product glycinin chain Ala #status predicted #label
GLA\
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S04603; JS0015
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Pred. No. 6.80e+00;
2; Mismatches 3
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Search completed: Fri Jun 11 17:58:45 1999 Job time: 83 secs.

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CLASSIFICATION
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#journal Plant Cell (1989) 1:313-328
#title Characterization of the glycinin gene family in soybean.
#cross-references MUID:92393391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors Sims, T.L.; Goldberg, R.B.
#Journal Nucleic Acids Res. (1989) 17:4386
##1tle The 91yCinin Gy(1) gene from soybean
#cross-references MUID:89296498
                                     318 TMRLRHNIGQTS 329
                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type DNA
                                                                                           Match 51.5%;
Local Similarity 58.3%;
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#experimental_source variety Dare
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#cross_references EMBL:X15121; NID:g18634; PID:g18635
 TMRTRHSTGGTN 15
                                                                                                                                                                                                                                                                             Gyl
96/1; 180/3; 366/3
#superfamily glycinin
storage protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Utsumi, S.; Kohno, M.; Mori, T.; Kito, M.:
J. Agric. Food Chem. (1987) 35:210-214
An alternate cDNA encoding glycinin Ala Bx subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S04603
                                                                                                                                                #product glycinin Bx chain *status predicted *label MAT3
#length 495 *molecular-weight 55706 *checksum 7917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S04603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nielsen, N.C.; Dickinson, C.D.;
Scallon, B.J.; Fischer, R.L.;
                                                                           Conservative
                                                                                                                                                                                                        #domain signal sequence #status predicted #label SIG\
#product glycinin Gl #status predicted #label MATI\
#product glycinin Ala chain #status predicted #label
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                                                                         Score 51; DB 2; I
Pred, No. 6.80e+00;
2; Mismatches 3
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Sims, T.L.; Drews, G.N.;
                                                                                                               Length 495
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:52:22 1999; MasPar time 2.45 Seconds 172.968 Million cell updates/sec

Tabular output not generated.

Title: >US-08-991-628-7
Description: (1-15) from US08991628.pep
Perfect Score: 9

Sequence: 1 QSGTMRTRHSTGGTN 15

Scoring table: PAM 150 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 24.516; Variance 27.383; scale 0.895

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

. 322221187 - 322221087	Result
0.000000000000000000000000000000000000	Score
100 550 550 550 550 550 550 550 550 550	% Query Match
1597 1597 1787 536 536 536 536 536 536 536 536 536 536	Length
	EG .
SOL_DROME SOL_DROME RPB1_EUPOC FYN_MOUSE FYN_WOUSE FYN_XENLA FYN_HUMAN TCPH_HUMAN TCPH_HUMAN GLC1_SOYBN GLC1_S	ID
DESMOGLEIN 3 PRECURSOR SMALL OPTIC LOBES PROT DNA-DIRECTED RNA POLYM PROTO-ONCOGENE TYROSIN T-COMPLEX PROTEIN 1, E PARA-AMINOBENZOATE SYN GLYCININ G1 PRECURSOR GLYCININ NINACIDIAL AMINOGENIC MIRACIDIAL AMINOGENIC LOCUS NOTCH 50S RIBOSOMAL PROTEIN SCYTALIONE DEHYDRAJASE TRANSCRIPTION INITIATI BINDIR PRECURSOR ORTHODASE (EC 3.2. CATALASE PRECURSOR (EC PROBABLE SERINE/THREON	Description
1.22e-01 2.09e-01 3.54e-01 3.54e-01 3.54e-01 3.54e-01 3.54e-01 1.67e+00 2.76e+00 2.76e+00 2.76e+00 2.76e+00 0.75e+00 1.19e+01 1.19e+01 1.19e+01 1.19e+01 1.19e+01 1.19e+01 1.19e+01 1.19e+01	Pred. No.

PIR; A41088; IJHUG3.
MIM; 169615; -5
PROSSITE; P500232; CADHERIN; PFAM; PF00028; Cadherin; 4.
HSSP; P09803; 1EDH.

RESULT	1
ก์ E	DSG3_HUMAN STANDAKU; PRT; 999 AA.
ĕ	(REL.
ää	35,
Ħ	GLEIN 3 PRECURSOR
ž	
ŏ	SAPIENS (HUMAN).
గ	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ĸ	PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
Ñ	[1]
¥	SEQUENCE FROM N.A.
×	MEDLINE; 92069753.
\$	AMAGAI M., KLAUS-KOVTUN V., STANLEY J.R.;
ä	"Autoantibodies against a novel epithelial cadherin in pemphigus
1 73	vulgaris, a disease of cell adhesion.";
£	
3 13	- I- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME CONCITIONS.
H 6	MEDIATING CELL-CELL ADHESION.
ដ	- i - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
검	-1- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL, OESOPHAGUS AND
ដ	
ဗ	-1- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
3 13	(POTENTIAL).
i	
88	DISEASE IN WHICH EPIDERMAL BLISTERS OCCUR AS THE RESULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES
ဂ	
ဂ	-!- SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS TO THE
င္ပ	DESMOSOMAL SUBFAMILY.
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ဂ	This SWISS-PROT entry is copyright. It is produced through a collaboration
88	ween the Swiss Institute of Bioinformatics and the EMBL outstation
18	European Bioinformatics Institute. There are no restrictions on
38	PS S
86	modified and this statement is not removed. Usage by and for commercial
88	entitles requires a license agreement (see http://www.isb-sib.ch/announce/
3 6	or send an email to licensewisd-sib.cn).
3 6	
另	EMBL; M76482; G190752;

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01-AUG-1992
01-NOV-1995
FLYBASE; FBgn0003464; sol.

PROSITE; PS00139; THIOL_PROTEASE_CYS;

PROSITE; PS00639; THIOL_PROTEASE_HIS;

PROSITE; PS00640; THIOL_PROTEASE_ASN;

PFAM; PF00641; zf-RanBP; 6.
                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                         brain gene of Drosophila melanogaster.";
PROC. NATL. ACAD. SCI. U.S.A. 88:7214-7218(1991).
-!- THE SOL (SMALL OPTIC LOBES) MUTATION ELIMINATES CERTAIN CLASSES
                                                                                                                                                                                                                                                                                                                                                                                                SOL_DROME
P27398;
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                                               EMBL; M64084; G158483; -. PIR; A41146; BVFFSL.
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                                                                                                                                                                                                                                                                                                                    DROSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
                                                                                                                                                                                                                                       'Molecular cloning and analysis of small optic lobes,
                                                                                                                                                                                                                                                    MIKLOS G.L.G.;
                                                                                                                                                                                                                                                             MEDLINE; 91334436.
DELANEY S.J., HAYWARD
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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IS OBSERVED, IN WHICH
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Similarity 100.0%;
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MEDINE; 3007138.

"Gene dosage as a possible major determinant for equal expression "Gene dosage as a possible major determinant for equal expression levels of genes encoding RNA polymerase subunits in the hypotrichous clilate Euplotes octocarinatus.";

NUCLEIC ACIDS RES. 20:4445-4450(1992).

-I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
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                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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ZN_FING
                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
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EUKARYOTA; ALVEOLATA; CILIOPHORA; HYPOTRICHS;
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                                                                                                                                                                                                                                                                                                                    TWELVE DIFFERENT POLYPEPTIDES. THIS POLYPEPTIDE IS THE LARGEST COMPONENT OF RNA POLYMERASE II.
SUBCELLULAR LOCATION: NUCLEAR.
THREE DISTINCT EURC-CONTAINING RNA POLYMERASES ARE FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE III FOR THE MRNA PRECURSOR, AND POLYMERASE III FOR 55
                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: EACH CLASS OF RNA POLYMERASE IS ASSEMBLED TWELVE DIFFERENT POLYPEPTIDES. THIS POLYPEPTIDE IS
                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
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                                        S33886; S33886.
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                  RNA_pol_A;
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24, LAST SEQUENCE UPDATE)
. 37, LAST ANNOTATION UPDATE)
POLYMERASE II LARGEST SUBUNIT
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BY SIMILARITY.
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Pred. No. 1.22e-01
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TRANSFERASE; DNA-DIRECTED

RNA

POLYMERASE; TRANSCRIPTION; ZINC; REPEAT;

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                                                                                                                                                                                                  PROSITE: PS00107; PROTEIN PROSITE: PS001109; PROTEIN PROSITE: PS50011; PROTEIN PROSITE: PS50001; SH2; 1.
PRAM: PF00017; SH2; 1.
PFAM: PF00018; SH3; 1.
PFAM: PF00018; SH3; 1.
PFAM: PF00019; PK1nase; 1
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Q05876;
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EUKARYOTA; METAZOA; CHORDATA;
NEOGNATHAE; GALLIFORMES; PHAS:
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01-FEB-1994 (REL.
01-OCT-1996 (REL.
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                                                                                                                                               PROTO-ONCOGENE; TRANSFERASE; ATP-BINDING; MYRISTYLATION;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: THYMUS AND SPLEEN.
SIMILARITY: CONTAINS 1 SH2 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN TYROSINE PHOSPHATE. SUBUNIT: ASSOCIATES THROUGH
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TISSUE SPECIFICIAN FIRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: IMPLICATED IN THE CONTROL CATALYTIC ACTIVITY: ATP + A PROTEIN
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PS50002; SH3; 1.
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PROTEIN_KINASE_DOM;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Inase, Yrk,
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Pred. No.
3; Misma
                 BY SIMILARITY.
MYRISTATE (BY:
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PALMITATE (BY:
SH3.
SH2.
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SH3 DOMAIN; SH2 DOMAIN; PA
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 PROTEIN KINASE
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IANIDAE; PHASIANINAE; GALLUS
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2.09e-01;
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( SIMILARITY).
( SIMILARITY).
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                                                                                                                                                 PALMITATE;
                                                                                                                                                                   PHOSPHORYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVES;
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Best Local S
Matches
                                                                                                                                                 PALMITOYLATION.
MEDLINE: 97345356.
WOLVEN A., OKAMURA H
"Palmitoylation of g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOD_RES
NP_BIND
BINDING
BINDING
ACT_SITE
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FYN_MOUSE P39688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FYN.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
EUKARYOTA; METAZOA; CHORDATA; MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P39688;
01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
         MEDLINE; 96251668.

GAUEN L.K.T., LINDER M.E., SHAW A.S.;

GAUEN L.K.T., LINDER M.E., SHAW A.S.;

"Multiple features of the p59fyn src homology 4 domain defi

"multiple features of the p59fyn src homology 4 domain defi

for immune receptor tyrosine-based activation motif (ITAM)

and for plasma membrane localization.";

J. CELL BIOL. 133:1007-1015(1996).

J. CELL BIOL. 133:1007-1015(1996).

I. CELL GROWTH.

-I- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +

PROTEIN TYROSINE PHOSPHATE.
                                                                                                                         "Painitoyiation of p59fyn is rever
membrane association.";
MOL. BIOL. CELL 8:1159-1173(1997).
                                                                                                                                                                                                     MEDLINE; 95071286.
KOSGI M., ZLATKINE P., LEY S.C
"Palmitoylation of multiple Sr
terminal motif.";
BIOCHEM. J. 303:749-753(1994).
                                                                                                                                                                                                                                                                             MEDLINE; 94019312.
SHENOY-SCARIA A.M., TIMSON L.K., KWONG J., SHAW A.S., LI "Palmitylation of an amino-terminal cysteine motif of protyrosine kinases p561ck and p59fyn mediates interaction glycosyl-phosphatidylinositol-anchored proteins."; MOL. CELL. BIOL. 13:6385-6392(1993).
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               COOKE M.P., PERLMUTTER R
"Expression of a novel f
hematopoietic cells.";
NEW BIOL. 1:66-74(1989).
                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED
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                                                                                                        YRISTOYLATION
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yn is reversible
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EMBL/GENBANK/DDBJ
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Pred.
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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DATA BANKS
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a homologous
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Best Local s
Matches
SEQUENCE FROM N.A.

MEDLINE; 90191723.

STEELE R.E., DENG J.C., GHOSN C.R.

"Structure and expression of fyn g
ONCOGENE 5:369-376(1990).

-!- FUNCTION: IMPLICATED IN THE CC.

-!- CATALYTIC ACTIVITY: ATP + A PF
PROTEIN TYROSINE PHOSPHATE.

-!- SUBUNIT: ASSOCIATES THROUGH IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; W27266; G309241; -.
EMBL; W70324; G1575677; -.
PIR; A44991, A44991
MGD; MGI:95602; FYN
MGD; MGI:95602; FYN
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1
PROSITE; PS50001; PROTEIN_KINASE_DOM; 1
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
PFAM; PF00017; SH2; 1.
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P13406;
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NP_BIND
BINDING
ACT_SITE
                                                                                                                                                01-JAN 1990 (REL. 13, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                          MESOBATRACHIA;
                                                                                                                   XENOPUS LAEVIS (AFRICAN CLAWED FROG) EUKARYOTA; METAZOA; CHORDATA; VERTEB
                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase;
HSSP; P06241; 1FYN.
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SIMILARITY: CONTAINS 1 SH2 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES
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                                                   GHOSN C.F
                                                                                                         DATA; VERTEBRATA; AMPHIBIA; BAG
PIPIDAE; XENOPODINAE; XENOPUS
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MYRISTATE.
PALMITATE.
PALMITATE.
SH3.
SH2.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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3.54e-01;
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 DOMAIN,
                     OF CELL GROWTH.
TYROSINE - ADP
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n Xenopus laevis
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                                                                                                                                                                                                                                                                                                              Length 533;
                                                                                                                                                  2.7.1.112) (P59-FYN).
 TO THE P85 SUBUNIT
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01-AUG-1992
01-FEB-1994
01-OCT-1996
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PFAM;
PFAM;
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PROSITE; PS50002; SH3; 1.
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                             STRAIN-RIO LANCETILLA;
MEDLINE; 91187435.
HANNIG G., OTTILIE S., SCH
"Conservation of structure
                                                                                                    XIPHOPHORUS HELLERI.
EUKARYOTA; METAZOA; CHOI
TELEOSTEI; EUTELEOSTEI;
                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M27502
PIR; A43806;
         in lower vertebrates.";
oncogene 6:361-369(1991)
                                                                       SEQUENCE
                                                                                           CYPRINODONTIFORMES;
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SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES
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PF00018; SH3; 1.
PF00069; pkinase;
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                                                                                                                                         (REL. 23, CREATED)
(REL. 28, LAST SEQUENCE UPDATE)
(REL. 34, LAST ANNOTATION UPDATE)
BURE TYROSINE-PROTEIN KINASE FYN (EC
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larity 57.1%;
Conservative
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TEI; ACANTHOPTERYGII;
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MYRISTATE (BY
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PALMITATE (BY
SH3.
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PHOSPHORYLATION (AUTO-)
                                                                                                              VERTEBRATA;
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expression
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1. No. 3.54e-01;
Mismatches 2
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                                                                                          POECILIDAE;
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OF CELL GROWTH
                                                                                                      ATHERINOMORPHA
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SEQUENCE FROM N.A.
MEDLINE; 86287278.
SEMBA K., NISHIZAWA M., MIYA.
YAMANASHI Y., SASAKI M., YAM.
"Yes-related protooncogene, ikinase family.";
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DOMAIN
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PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
HSSP; P06241; 1AOT.
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                                                                                                                                                                        01-JAN-1988 (REL. 06, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (EC
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                                                                                                               HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
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SIMILARITY: CONTAINS 1 SH2 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
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PS00109; PROTEIN_KINASE_TYR;
PS50011; PROTEIN_KINASE_DOM;
PS50001; SH2; 1.
PS50002; SH3; 1.
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SH2.
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PHOSPHORYLATION
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 MYRISTOYLATION, AND PHOSPHORN MEDLINE; 91016431.
PETERS D.J., MCGREW B.R., PEI "In vivo phosphorylation and oncogene product in IM-9 huma ONCOGENE 5:1313-1319(1990).
                                                                                                                                                                                                                                                                                   MEDLINE; 97121261.

RENZONI D.A., PUGH D.J., SILIGARDI G., DAS P., WATERFIELD M.D., CAMPBELL I.D., LADBURY J.E.;

"Structural and thermodynamic characterization the SH3 domain from Fyn with the proline-rich be subunit of PI3-kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "High-resolution crystal structures of complexed with proline-rich peptides."; NAT. STRUCT. BIOL. 1:546-551(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 87089775. KAWAKAMI T., PENNI
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MUSACCHIO A., SARASTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAWAKAMI T., PENNINGTON C.Y., ROBBINS "ISolation and oncogenic potential of MOL. CELL. BIOL. 6:4195-4201(1986).
STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAMPBELL I.D.;
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MEDLINE; 96279837.
LEE C.H., SAKSELA K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spectrin.";
EMBO J. 12:2617-2624(1993)
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                                                                                    RUDD
                                                                                                                                                                      MULHERN T.D., SHAW G.L., MORTON C.J., DAY "The SH2 domain from the tyrosine kinase is phosphotyrosyl peptide reveals insights in binding specificity.";
                                                                                                                                                                                                   MEDLINE; 98035454
MULHERN T.D., SHA
"The SH2 domain f
                                                                                                                                                                                                                                                STRUCTURE BY NMR OF SH2
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MORTON C.J., PUGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEE C.H., SAKSELA K., MIRZ.
"Crystal structure of the a
a Src family SH3 domain.";
CELL 85:931-942(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOBLE M.E.M.,
                                                                                                                BINDING OF SH3 DOMAIN TO PI 3-KINASE MEDLINE; 93348274.
                                                                                                                                                            STRUCTURE
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                                                                                                    PRASAD
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PFAM; PF000018; SH3; 1.
PFAM; PF000069; PK1nase; 1.
PROTO-ONCOGENE; TRANSFERASE; T
ATP-BINDING; MYRISTYLATION; SH
LIPOPROTEIN; 3D-STRUCTURE.
                                                                                                                                                                                                                                                                                                                                                                                          MIM; 1370
PROSITE;
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EMBL; M14676; G338228;
PIR; A24314; TVHUSY.
PIR; A25389; TVHUSR.
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les 8; Conser
   71 HTGTLRTRGGTGVT
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SIMILARITY: CONTAINS 1 SH2 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: TO OTHER PROTEIN TYROSINE KINASES
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ween the Swiss Institute of Bioinfo
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1NYF; 08-NOV-96.
1NYG; 08-NOV-96
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PS50002; SH3; 1.
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PS00109; PROTEIN_KINASE_TYR;
PS50011; PROTEIN_KINASE_DOM;
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                              55.6%;
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                   Score 55; DB 1;
Pred. No. 3.54e-01
4; Mismatches
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PALMITATE
PALMITATE
SH3.
SH2.
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SH3 DOMAIN; SH2 DOMAIN; PALMITATE;
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A -> R (IN REF. :
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BY SIMILARITY.
PHOSPHORYLATION (AUTO-)
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                                            01B18DD0 CRC32;
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                                      Length 536;
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4.1.3.-) (ADC SYNTHASE).

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CHAPERONE;
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PROSITE; PS00751; 1
PROSITE; PS00995; 1
PROSITE; PS00995; 1
PFAM; PF00118; cpnf
PFAM; PF00118; cpnf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FURUSHI M., KIMURA I., YAMAMOTO N.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

-I FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF
ATP HYDROLYSIS. KNOWN TO PLAY A ROLE, IN VITRO, IN T
ACTIN AND TUBULIN (BY SIMILARITY).

-I SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 9
FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER (BY
-I SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-I SUBCELLULAR LOCATION: THE TCP-1 CHAPERONIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCPH_HUMAN STANDARD; PRT; 543 AA.

(99832; O1487];
(01-NOV-1997 (REL. 35, CREATED)

15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)

15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)

17-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) (HIV-1

INTERACTING PROTEIN).

CCT7 OR CCTH OR NIP7-1.

HOMO SAPIENS (HUMAN).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
PABB_STRLI STANDARD; PRT; 475 AA. P27630; 01-AUG-1992 (REL. 23, CREATED) 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE) 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE) PARA-AMINOBENZOATE SYNTHASE COMPONENT I (EC 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. WON K.-A., REED S.I.; SUBMITTED (NOV-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 13-424 FROM N.A. FUKUSHI M., KIMURA T., YAMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF026292; G2559010; -. EMBL; U83843; G1800303; -.
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543
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336
364
374
407
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'51; TCP1_2; 1.
'95; TCP1_3; 1.
'cpn60_TCP1; 1.
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36, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) (HIV-1
                                                                                                                                                                                                                                                                                                  52.5%;
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L -> P (IN REF. 2).
A -> P (IN REF. 2).
C -> L (IN REF. 2).
LRG -> SPC (IN REF. 2).
A -> P (IN REF. 2).
A -> P (IN REF. 2).
A -> P (IN REF. 2).
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Pred. No. 1.67e+00;
3; Mismatches 1.
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Query Match
Best Local Similarity 58.3%;
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476
481
303
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STRAIN-CV. BONMINORI;
MEDLINE; 86041867.
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297
477
477
107
381 AA;
DISULFIDE BOND
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GLC1_SOYBN
P04776;
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                                                                                                     SEQUENCE FROM N.A.

STRAIN-66 / 1326;

MEDLINE; 93231526.

A RHIN F.F., VINING L.C.;

Corganization of the genes encoding p-aminobenzoic acid synthetase from Streptomyces lividans 1326.";

GENE 126:129-133(1993).

CADC) FROM CHORISMATE AND GLUTAMINE.

CADC, FROM CHORISMATE AND GLUTAMINE.

CADC, FROM CHORISMATE STRE BIOSYNTHESIS OF 4-AMINO-4-DEOXYCHORISMATE CADC.

CADC, PROM CHORISMATE NO GLUTAMINE.

BLOSYNTHESIS OF P-AMINOBENZOATE (PABA).

CATALYZES THE FORMATION OF ADC BY BINDING CHORISMATE AND AMMONIA;

CATALYZES THE FORMATION OF ADC BY BINDING CHORISMATE AND AMMONIA;

COMPONENT II PROVIDES THE GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
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GIXBARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
FABALES; FABACEAE; PAPILIONOIDEAE; GLYCINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIEESEN N.C., DICKINSON C.D., CHO T.-J., THANH V.H., SCALLON B.J., FISCHER R.L., SIMS T.L., DREWS G.N., GOLDBERG R.B.; "Characterization of the glycinin gene family in soybean."; PLANT CELL 1:313-328(1989).
-i- FUNCTION: GLYCININ IS THE MAJOR SEED STORAGE PROTEIN OF SOYBEAN.
-i- SUBBUNIT: HEXAMER; EACH SUBBUXI IS COMPOSED OF AN ACIDIC AND A BASIC CHAIN DERIVED FROM A SINGLE PRECURSOR AND LINKED BY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                      STREPTOMYCES LIVIDANS.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; STREPTOMYCINEAE; STREPTOMYCETACEAE; STREPTOMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLC3_SOYBN STANDARD; PRT; 481 AA.
P118728;
01-0CT-1989 (REL. 12, CREATED)
01-0CT-1989 (REL. 12, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GLYCININ G3 PRECURSOR (CONTAINS: GLYCININ A SUBUNIT; GLYCININ B
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Pred. No. 2.76e+00;
4; Mismatches 4; Indels
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STRAIN-CV, DARE; TISSUE-LEAF;
MEDLINE; 89296500.
CHO T.-J., NIELSEN N.C.;
"The glycinin Gy3 gene from soybean.";
NUCLDIC ACIDS RES. 17:4388-4388(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00425; chorismate_bind; 1.
LYASE; FOLATE BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 42.9%;
Matches 6; Conservative
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EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLLOPHYTA; EUDICOTYLEDONS; ROSIDAE;
FABALES; FABACEAE; PAPILIONOIDEAE; GLYCINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEGORO T., MOMMA T., FUKAZAWA C.;
"A cDNA clone encoding a glycinin Ala subunit precursor of soybean.";
NUCLEIC ACIDS RES. 13:6719-6731(1985).
SIMILARITY: BELONGS TO THE 11S SEED STORAGE PROTEINS (GLOBULINS) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GLYCININ G1 PRECURSOR (CONTAINS: GLYCININ A1A SUBUNIT; GLYCININ BX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDILINE; 92393391.
NIELSEN N.C., DICKINSON C.D., CHO T.J., THANH V.H., SCALLON B.J.,
NIELSEN K.L., STMS T.L., DREWS G.N., GOLDBERG R.B.;
"Characterization of the glycinin gene family in soybean.";
PLANT CELL 1:313-328(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 51; DB 1; Length 481;
Pred. No. 2.76e+00;
2; Mismatches 3; Indels
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UTSUNI S., KOHNGTM., MORI T., KITO'M.;
"An alternate CDNA encoding glycinin Ala Bx subunit.";
"A. AGRIC. FOOD CHEM. 35:210-214(1987).
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X15123; G18639; --
PIR; S04605; S04605.
PROSITE: PS001305; 115_SEED_STORAGE; 1.
SPRAY; PF00190; Seedstore_l1s; 1.
SEED STORAGE PROTEIN; MULTIGENE FAMILY; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A SUBUNIT.
B SUBUNIT.
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"The glycinin Gyl gene from soybean.";
NUCLEIC ACIDS RES. 17:4386-4386(1989).
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SEQUENCE FROM N.A.
STRAIN-CV. DARE; TISSUE-LEAF;
MEDLINE; 89296498.
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EMBL; X15121; G18635; -.
EMBL; X2985; G18615; -.
PIR; A23497; FWSYG2.
PIR; S04603; S04603
PIR; S04603; S04603
PIR; S04603; S10851.
                                                                                                                                                                                                    MA5D_SCHJA
P13411;
01-JAN-1990
C1-JAN-1990
15-JUL-1998
IMMUNOGENIC
    This SW
between
                                 MEDLINE; 89261924.

SCALLON B.J., BOGITSH B.J., CARTER C.E.;

"Characterization of a large gene family in Schistosoma japane and the encodes an immunogenic miracidial antigen.";

MOL. BIOCHEM. PARASITOL. 33:105-112(1989).

-I- DEVELOPMENTAL STAGE: MIRACIDIA.

-I- SIMILARITY: NEARLY IDENTICAL TO IMMUNOGENIC MIRACIDIAL ANTIGENS 81', 81 AND 8C.
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CONFLICT
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STRAIN-PHILIPPINE;
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                                                                                                                                                          EUKARYOTA; METAZOA;
SCHISTOSOMATOIDEA;
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- SUBUNIT: HEXAMER; EACH
BASIC CHAIN DERIVED ID DISULFIDE BOND.
- PIM: THE PRECURSOR IS
                                                                                                                                                                                                                                                                                                         4 IMRTRHSTGGTN 15
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  SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                      (REL. 13, C) (REL. 13, L) (REL. 36, L) (REL. 36, L)
                                                                                                                                                         JAPONICUM (BLOOD FLUKE).
METAZOA; PLATYHELMINTHES;
TOIDEA; SCHISTOSOMATIDAE;
                                                                                                                                                                                                                                                                                                                                                  51.5%;
larity 58.3%;
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ROTEIN; MULTIGENE FAMILY;
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L ANTIGEN 5D (FRAGMENT).
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Pred. No. 2.76e+00
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SCHISTOSOMA
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                                                                                                                                                                       This SWISS-PROT entry is copyright, It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
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01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
01-APR-1993 (REL. 27, LAST ANNOTATION UPDATE)
AMINOCICOSIDE N3'-ACETYLTRANSFERASE TYPE VII
CAMINOCYCLITOL 3-N-ACETYLTRANSFERASE TYPE VII
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 91285425.
SALAUZE D., PEREZ-GONZALEZ J.A., PIEPERSBERG W., DAVIES J.;
"Characterisation of aminoglycoside acetyltransferase-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                              STREPTOMYCES FRADIAE.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; STREPTOMYCINEAE; STREPTOMYCES
                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                   -i- FUNCTION: RESISTANCE TO NEOMYCIN.
-i- CATALYTIC ACTIVITY: ACETYL-COA + A 2-DEOXYSTREPTAMINE
- COA + N3'-ACETYL-2-DEOXYSTREPTAMINE ANTIBIOTIC.
-i- SIMILARITY: TO OTHER AAC(3) PROTEINS.
                                                                                                                                                                                                                                                                                                                                          GENE 101:143-148(1991)
                                                                                                                                                                                                                                                                                                                                                                  of neomycin-producing Micromonospora chalcea
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1; Mismatches !
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HEMA_PI3B P06167; 01-JAN-1988 01-JAN-1988 01-OCT-1996

(REL. 06, CREATED)
(REL. 06, LAST SEQUENCE UPDATE)
(REL. 34, LAST ANNOTATION UPDATE)

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STANDARD;

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                                                          Query Match 50.5%;
Best Local Similarity 61.5%;
Matches 8; Conservative
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MEDLINE; 87174819.

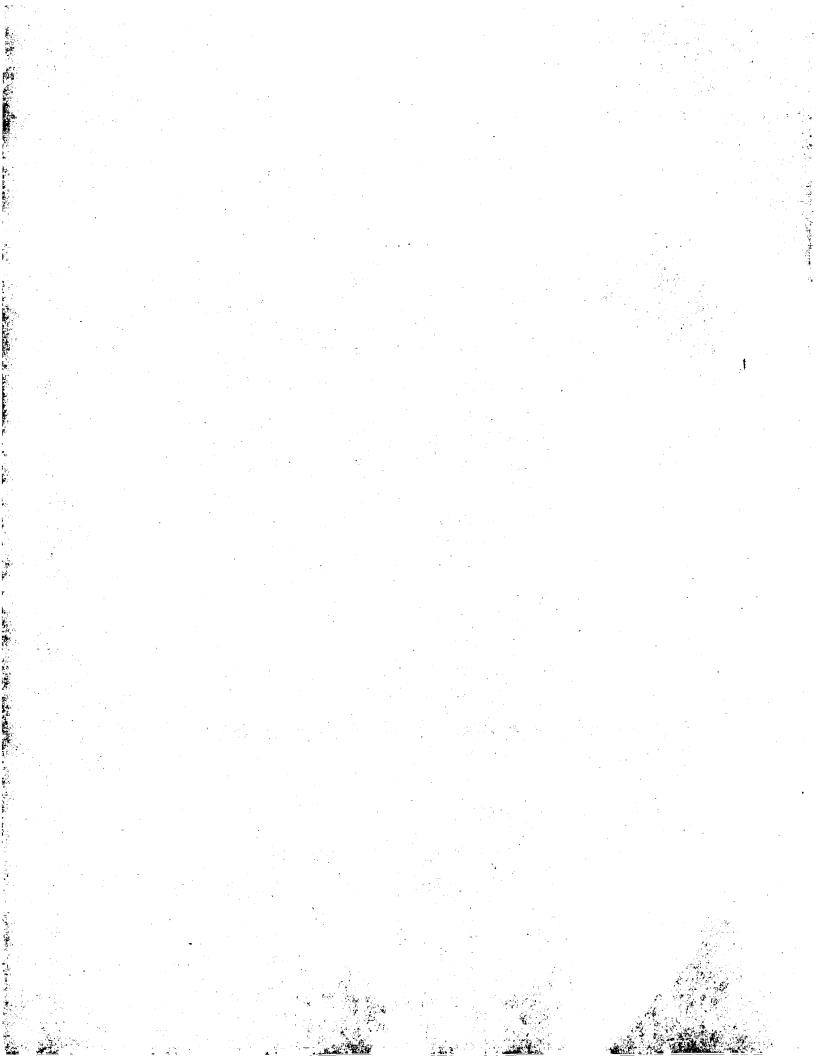
SUZU S., SAKAI Y., SHIDDA T., SHIBUTA H.;

NUCLEOCTION SEQUENCE OF the bovine parainfluenza 3 v1rus genome: the genes of the F and HN glycoproteins.";

NUCLEIC ACIDS RES. 15:2945-2958(1987).

-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEUROAMINIDASE ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING THE MATURE VIRIONS FROM THE NEURAMNINIC ACID CONTAINING
                                                                                                                                                                                                                            TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its up non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
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-1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BOVINE PARAINFLUENZA 3 VIRUS.
VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES;
PARAMYXOVIRIDAE; PARAMYXOVIRINAE; PARAMYXOVIRUS.
                                                                                                                                                                                                                                                                                                       EMBL; Y00114; G60897; -..
EMBL; D84095; G1255658; -.
PIR; B27218; HNNZB3.
PFAM; PF00423; HN; 1.
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                                                                                                                                                                                                                                                            TRANSMEMBRANE.
                                                                                                                                                                                                                                                                                           YDROLASE; HEMAGGLUTININ; ENVELOPE PROTEIN; GLYCOPROTEIN;
18 GTTRDRHSSKATN 30
|| | || ||:::||
3 GTMRTRHSTGGTN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEURAMINIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLYCOPROTEINS.
                                                                                                                              448
523
570
572 AA;
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572
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351
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523
                                                                                                                                64590 MW;
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                               Score 50; DB 1; Length 572; Pred. No. 4.53e+00; 2; Mismatches 3; Indels
                                                                                                                             PÓTENTIAL.
'876CFFE6 CRC32;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:54:53 1999; MasPar time 6.10 Seconds 134.225 Million cell updates/sec

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Description: Perfect Score: Sequence: Title: >US-08-991-628-7 (1-15) from US08991628.pep 99

QSGTMRTRHSTGGTN 15

Scoring table: РАМ 150 Gap 15

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 24.193; Variance 26.150; scale 0.925

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

20	18	17	16	15	14	13	12	11	10	9	8	7	S	Մ	4	ω	N	~	Result
51	52	52	52	53	53	53	53	53	53	53	54	54	54	55	55	57	62	87	Score
51.5	52.5	52.5	52.5	. 53.5	53.5	53.5	53.5	53.5	53.5	53.5		54.5	54.5	55.6	55.6	57.6	62.6	87.9	Query Match
69	1042	153	136	844	469	469	161	160	160	160	859	839	776	537	534	1597	421	993	Length
14	ı	N	N	v	14	14	9	9	9	9	11	11	11	11	4	G	N	11	8
P90363	P90974	069604	051792	044476	P88838	P88837	080273	021920	Q38226	080162	088509	088510	088511	Q62844	Q16248	061346	086590	035902	ID
GLYCOPROTEIN B (FRAGME	ADM-1 PREPROPROTEIN PR	TRANSPOSASE IS1355.	HYPOTHETICAL 14.7 KD P	E04A4.4 PROTEIN.	NEURAMINIDASE.	NEURAMINIDASE.	MIDDLE EXPRESSED M1, M	HYPOTHETICAL 18.0 KD P	ORF3.	COMPLETE GENOME.	DNA CYTOSINE-5 METHYLT	DNA CYTOSINE-5 METHYLT	DNA CYTOSINE-5 METHYLT	PROTO-ONCOGENE FYN.	P59FYN.	SMALL OPTIC LOBES.	PUTATIVE SECRETED PROT	DESMOGLEIN 3 (FRAGMENT	Description
3.82e+00	2.26e+00	2.26e+00	2.26e+00	1.33e+00	1.33e+00	1.33e+00	1.33e+00	1.33e+00	1.33e+00	1:33e+00	7.76e-01	7.76e-01	7.76e-01	4.50e-01	4.50e-01	1.48e-01	8.35e-03	9.09e-10	Pred. No.

45	44	43	42	41	40	39	38	37	36	35 35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	77
49	49	49	49	49	49	49	49	49	49	49	50	50	50	ઝુ	50	51	51	51	51	51	51	51	51	5
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Q94279	P91905	015017	035412	060081	043166	Q25289	Q61895	Q61642	007863	Q45261	Q65689	Q53827	Q22250	Q44378	011346	Q69173	044536	Q69174	P90394		P90392	P90393	Q68570	76706d
PARTIAL CDS.	RYANODINE RECEPTOR.	KIAA0299 (FRAGMENT).	SPA-1 LIKE PROTEIN P12	HYPOTHETICAL 171.2 KD	KIAA0440 (FRAGMENT).	MAJOR SURFACE GLYCOPRO	PRECURSOR.	HISTOCOMPATIBILITY 2,	RPKA.	NOD L.	HEMAGGLUTININ-NEURAMIN	CEPHALOSPORIN C HYDROX	T06D8.3 PROTEIN.	VIRULENCE PROTEIN.	CLONE H1-41 HOMOLOG OF	GLYCOPROTEIN B:	COSMID H22D07.	GLYCOPROTEIN B (FRAGME	GLYCOPROTEIN B VARIABL	GLYCOPROTEIN B VARIABL	GLYCOPROTEIN B VARIABL		GLYCOPROTEIN B (FRAGME	GLYCOPROTEIN B (FRAGME
1.05e+01	1.06e+01	1.06e+01	1.06e+01	1.06e+01	1.06e+01	1.06e+01	1.06e+01	1.06e+01	1.06e+01	1.06e+01	6.40e+00	6.40e+00	6.40e+00		6.40e+00	3.82e+00	3.82e+00	3.82e+00	3.82e+00	3.82e+00			3.82e+00	٠

OCCUPATO OCC	Db Qy RESULT	Qu Ma	DR DR KW	CC RR RR RR	8 0 0 0 g	RESULT
01-NOV-1998 (TREMBLREL. 08, CREATED) 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) PUTATIVE SECRETED PROTEIN. SC2H4.07C. STREPTOMYCES COELICOLOR. BACTERIA; FIRMICUTES, ACTINOBACTERIA; ACTINOBACTERIDAE; ACTINOMYCETALES; STREPTOMYCINEAE; STREPTOMYCES.	743 SGTMRTRHSTGGT 755	Query Match 87.9%; Score 87; DB 11; Length 993; Best Local Similarity 100.0%; Pred. No. 9.09e-10; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	PROSITE; PS00232; CADHERIN; 2. PRAM; PF00028; cadherin; 4. CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; CALCIUM-BINDING; REPEAT. NON_TER 993 993 SEQUENCE 993 AA; 107888 MW; 881794BD-CRC32;	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-BALB/C; STRAIN-BALB/C; ISHIKAWA H., LI K., UITTO J.; SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. FINEL: SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY). FINEL: UBSG16. G2293230: -	DSG3. MUS MUSCULUS (MOUSE). MUS MUSCULUS (MOUSE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.	O35902 PRELIMINARY; PRT; 993 AA. O35902; O1-JAN-1998 (TREMBLREL. 05, CREATED) O1-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE) O1-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) DESMOGLEIN 3 (FRAGMENT).

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SEQUENCE FROM N.A.
STRAIN=A3(2);
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01-AUG-1998
01-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 96129280.

DE COUET H.G., FONG K.S., WEEDS A.G., MCLAUGHLIN P.J., MIKLOS G.
"Molecular and mutational analysis of a gelsolin-family member
encoded by the flightless I gene of Drosophila melanogaster.";
GENETICS 141:1049-1059(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REDENBACH M., KIESER H.M., DENAPAITE D., EICHNER A., KINASHI H., HOPWOOD D.A.;

"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

MOL. MICROBIOL. 21:77-96(1996).

EMBL; AL031514; E1319225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARKHILL J., BARRELL SUBMITTED (SEP-1998)
                                                                                                                                MALESZKA R., DE COUET H.G., MIKLOS G.L.G:;
PROC. NATL. ACAD. SCI. U.S.A. 0:0-0(1998).
EMBL; AF01777; G3004662; -.
SEQUENCE 1597 AA; 174696 MW; C6C4952E
                                                                                                                                                                                                                                                                                    MIKLOS G.L., YAMAMOTO M., BURNS R.G., MALESZKA R.; "An essential cell division gene of Drosophila, absent from Saccharomyces, encodes an unusual protein with tubulin-like myosin-like peptide motifs."; PROC. NATL. ACAD. SCI. U.S.A. 94:5189-5194(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-CANTONS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DROSOPHILIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DROSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSE
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMALL OPTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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873 SGAIPKRHSTGGS 885
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                                        h 57.6%;
Similarity 61.5%;
8; Conservative
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Pred. No.
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                      Score 57; DB 5; I
Pred. No. 1.48e-01;
3; Mismatches 2
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                                                                                     Length 1597;
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Q16248;
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01-NOV-1996
                                                                                                                                                                                                                                           TISSUE-WHOLE BRAIN;

NEMOTO K., SEKIMOTO M., KAGEYAMA H., FUKAN
UEYAMA T., SENBA E., TOMITA I.;

SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDBJ
EMBL; U35365; G1101768; -

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
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Q62844;
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RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAGOA; CHORDATA; VE
SCIUROGNATHI; MURIDAE; MURINAE;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TREMBLREL. 01, 01-NOV-1996 (TREMBLREL. 01, 01-NOV-1998 (TREMBLREL. 08,
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SEQUENCE 534
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                                                                                                                                                             PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
SEQUENCE 537 AA; 60701;
                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-SHRSP STROKE-PRONE SPONTANEOUSLY HYPERTENSIVE
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PFAM; PF00018; SH3; 1.
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1 QSGTMRTRHSTGGT
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BL; S74774; G80205
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                                                                               Similarity 57.1%;
8; Conservative
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534 AA; 60226
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57.1%;
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AE; MURINAE; RATTUS.
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                                                                                                 Score 55;
Pred. No.
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Pred. No.
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                                                                                  Mismatches
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                                                                           534
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4.50e-01;
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SEQUENCE FROM N.A.

A OKANO M., XIE S., LI E.;

A OKANO M., XIE S., LI E.;

Cytoning and characterization of a fa

AT (Cytosine-5) methyltransferases.";

RL NAT. GENET. 19.219-220(1998).

BR EMBL, AF068627, G3327982;

KW TRANSFERASE; METHYLTRANSFERASE.

**POHENCE 839 AA; 94798 MW; BD2A

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OKANO M., XIE S., LI E.;

"Cloning and characterization of a factorization of a factoriz
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MUS MUSCULUS
EUKARYOTA; ME'
DIMT3B.
MUS MUSCULUS (MOUSE)
THEARYOTA; METAZOA;
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MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VI
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O88510;
O1-NOV-1998 (TREMBLREL 08, CREATED)
O1-NOV-1998 (TREMBLREL 08, LAST SEQUENCE UPDATE)
O1-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)
DNA CYTOSINE-5 METHYLTRANSFERASE 3B2.
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01-NOV-1998 (TREMBLREL. 08, LAST
01-NOV-1998 (TREMBLREL. 08, LAST
DNA CYTOSINE-5 METHYLTRANSFERASE
                                                                                                                                       01-NOV-1998 (TREMBLREL 08, CREATED)
01-NOV-1998 (TREMBLREL 08, LAST 520
01-NOV-1998 (TREMBLREL 08, LAST ANN
DNA CYTOSINE-5 METHYLTRANSFERASE 3B1
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QSGTMRTRHSTGGTN
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QSGTMRTRHSTGGTN 15
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Similarity 46.7%;
7; Conservative
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METAZOA; CHORDATA; VERTEBRATA;
HT: MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                           CHORDATA;
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                               VERTEBRATA;
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SUBMITTED (AUG-1998) TO EMBL/GENBANK/DDBJ DATA BA EMBL; AF087814; G3695269; -.
SEQUENCE 161 AA; 18213 MW; BAC5B605 CRC32:
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HYPOTHETICAL PROTEIN.
SEQUENCE 160 AA; 17990 MW; 9D027B4F CRC32;
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RINCE A., FITZGERALD G.F.;
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044476; PRELIMINARY;
044476; QTREMBLREL 06, C
01-JUN-1998 (TREMBLREL 06, C
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E0444-4 PROTEIN.
                   SEQUENCE FROM N.A.
STRAIN-BRISTOL.N2;
MEDLINE; 94150718.
WILSON R., AINSCOPER R.,
BONFIELD J., BURTON J., C
CRAXTON M., DEAR S., DU Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genetic characterisation of an influenza (HIN7) isolated from pigs in England."; ARCH. VIROL. 142:1045-1050(1997). EMBL; U8589; G1835742; -. FFAM; PF00064; neur; 1
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PFAM: PFO0064; neur: 1.
SEQUENCE 469 AA; 51888 MW; 3FB1AOA5 CR
                                                                                                                                                                  CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
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01-MAY-1997 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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MEDLINE; 97335203.
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VIRUSES; SSRNA NEGATIVE-STRAND
INFLUENZA VIRUS A AND B GROUP.
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    GARDNER
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, ANDERSON K., BAYNES C.,
CONNELL M., COPSEY T., CO
Z., DURBIN R., FAVELLO A
AWKINS T., HILLIER L., JI
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LAST SEQUENT LAST ANNOTED
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Pred. No. 1.33e+00;
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LO A., FULTON I
, JIER M., JOHI
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RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMUTRAY A., MORTINGE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERY.MIZG J., THOMAS K., VADDIN M., VAUGHAN K., WATERSTON R.,
RA THIERY S68:32-38(1994).
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT Glegans.",
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT NATURE 368:32-38(1994).
RT SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA SAMMONS L., WOHLDMANN P., BIEWALD T.;
RI SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RN SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RN WATERSTON R.;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
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RN SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
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